

50	55	60													
Pro	Gly	Ala	Asp	Ser	Ala	Ala	Pro	Ala	Ser	Ile	Met	Val	Phe	Asp	Asp
55	70	75	80												
Met	His	Val	Ala	Pro	Arg	Val	Ile	Phe	Ieu	Pro	Gly	Pro	Ala	Ala	Ala
60	65	70	75	80	85	90	95								
Ieu	Thr	Ser	Asp	Asp	His	Gly	Thr	Ala	Phe	Ieu	Ala	Ala	Arg	Gly	Gly
65	70	75	80	85	90	95	100	105	110						
Tyr	Phe	Val	Ala	Asp	Leu	Ser	Ser	Gly	His	Thr	Ala	Arg	Val	Asn	Val
70	75	80	85	90	95	100	105	110	115	120	125	130	135	140	
Ala	Asp	Ala	Ala	His	Thr	Asp	Phe	Thr	Ala	Ile	Ala	Ala	Ala	Ala	Ala

(2) INFORMATION FOR SEQ ID NO:277:

SEQUENCE CHARACTERISTICS

- (A) LENGTH: 142 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(11) MOLECULE TYPE: protein

(X4) SEQUENCE DESCRIPTION: SEQ ID NO:277:

```

Met His Ile Thr Leu Asn Ala Ile Leu Arg Ala Ile Phe Gly Ala Gly
      5          10          15
Gly Ser Glu Leu Asp Glu Leu Arg Arg Leu Ile Pro Pro Trp Val Thr
      20          25          30
Leu Gly Ser Arg Leu Ala Ala Leu Pro Lys Pro Lys Arg Asp Tyr Gly
      35          40          45
Arg Leu Ser Pro Trp Gly Arg Leu Ala Glu Trp Arg Arg Glu Tyr Asp
      50          55          60
Thr Val Ile Asp Glu Leu Ile Glu Ala Glu Arg Ala Asp Pro Asn Phe
      65          70          75          80
Ala Asp Arg Thr Asp Val Leu Ala Leu Met Leu Arg Ser Thr Tyr Asp
      85          90          95
Asp Gly Ser Ile Met Ser Arg Lys Asp Ile Gly Asp Glu Leu Leu Thr
      100         105         110
Leu Leu Ala Ala Gly His Glu Thr Thr Ala Ala Thr Trp Ala Gly Arg
      115         120         125
Ser Asn Gly Ser Thr Gly Thr Pro Thr Cys Ser Arg Leu Trp
      130         135         140

```

INFORMATION FOR SEC ID NO: 278

SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 163 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

MOLECULAR TYPE: process

(b) SEQUENCE DESCRIPTION: SEQ ID NO: 270:

Val Leu Val Ala Gly Cys Ser Ser Asn Pro Leu Ala Asn Phe Ala Pro
 1 5 10 15
 Gly Tyr Pro Pro Thr Ile Glu Pro Ala Gln Pro Ala Val Ser Pro Pro
 20 25 30
 Thr Ser Gln Asp Pro Ala Gly Ala Val Arg Pro Leu Ser Gly His Pro
 35 40 45
 Arg Ala Ala Leu Phe Asp Asp Gly Thr Arg Gln Leu Val Ala Leu Arg
 50 55 60
 Pro Gly Ala Asp Ser Ala Ala Pro Ala Ser Ile Met Val Phe Asp Asp
 65 70 75 80
 Val His Val Ala Pro Arg Val Ile Phe Leu Pro Gly Pro Ala Ala Ala
 85 90 95
 Leu Thr Ser Asp Asp His Gly Thr Ala Phe Leu Ala Ala Arg Gly Gly
 100 105 110
 Tyr Phe Val Ala Asp Leu Ser Ser Gly His Thr Ala Arg Val Asn Val
 115 120 125
 Ala Asp Ala Ala His Thr Asp Phe Thr Ala Ile Ala Arg Arg Ser Asp
 130 135 140
 Gly Lys Leu Val Leu Gly Ser Ala Asp Gly Ala Val Tyr Thr Leu Ala
 145 150 155 160
 Lys Asn Pro

(2) INFORMATION FOR SEQ ID NO:279:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 240 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(2) MOLECULE TYPE: protein

(3) SEQUENCE DESCRIPTION: SEQ ID NO:279:

Trp Gly Ala Pro Pro Ser Gly Gly Pro Ser Pro Trp Ala Gln Thr Pro
 1 5 10 15
 Arg Lys Thr Asn Pro Trp Pro Leu Val Ala Gly Ala Ala Ala Val Val
 20 25 30
 Leu Val Leu Val Leu Gly Ala Ile Gly Ile Trp Ile Ala Ile Arg Pro
 35 40 45
 Lys Pro Val Gln Pro Pro Gln Pro Val Ala Glu Glu Arg Leu Ser Ala
 50 55 60
 Leu Leu Leu Asn Ser Ser Glu Val Asn Ala Val Met Gly Ser Ser Ser
 55 70 75 80
 Met Gln Pro Gly Lys Pro Ile Thr Ser Met Asp Ser Ser Pro Val Thr
 85 90 95
 Val Ser Leu Pro Asp Cys Gln Gly Ala Leu Tyr Thr Ser Gln Asp Pro
 100 105 110
 Val Tyr Ala Gly Thr Gly Tyr Thr Ala Ile Asn Gly Leu Ile Ser Ser
 115 120 125
 Glu Pro Gly Asp Asn Tyr Glu His Trp Val Asn Gln Ala Val Val Ala
 130 135 140
 Phe Pro Thr Ala Asp Lys Ala Arg Ala Phe Val Gln Thr Ser Ala Asp
 145 150 155 160

Lys Trp Lys Asn Cys Ala Gly Lys Thr Val Thr Asn Lys Ala
 145 176 175
 Lys Thr Tyr Arg Trp Thr Phe Ala Asp Val Lys Gly Ser Pro Pro Thr
 180 185 190
 Ile Thr Val Ile Asp Thr Gln Glu Gly Ala Glu Gly Trp Glu Cys Gln
 195 200 205
 Arg Ala Met Ser Val Ala Asn Asn Val Val Val Asp Val Asn Ala Cys
 210 215 220
 Gly Tyr Gln Ile Thr Asn Gln Ala Gly Gln Ile Ala Ala Lys Ile Cys
 225 230 235 240

(2) INFORMATION FOR SEQ ID NO:280:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:280:

Asp Val Val Glu Ala Ala Ile Ala Arg Ala Glu Ala Val Asn Pro Ala
 1 5 10 15
 Leu Asn Ala Leu Ala Tyr
 20

(2) INFORMATION FOR SEQ ID NO:281:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 174 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:281:

Leu His Pro Ala Gly Ala Thr Asn Gly Ser Gly Gln Leu Ala Leu Pro
 1 5 10 15
 Val Glu Ala Pro Pro Arg Ser Val Pro Ser His Gly Glu Pro Leu Gly
 20 25 30
 Ser Ala Ala Pro Glu Gly Leu Glu Gly Glu Phe Asp Asp Arg Ile Asp
 35 40 45
 Glu Arg Phe Pro Val Phe Ser Ser Ala Ser Leu Ala Glu Ala Leu Pro
 50 55 60
 Gly Pro Leu Thr Pro Met Thr Leu Asp Val Gln Leu Ser Gly Leu Arg
 65 70 75 80
 Ala Ala Gly Arg Ala Met Gly Arg Val Leu Ala Leu Gly Gly Val Val
 85 90 95
 Ala Asp Glu Trp Glu Arg Arg Ala Ile Ala Val Phe Gly His Arg Pro
 100 105 110
 Tyr Ile Gly Val Ser Ala Asn Ile Val Ala Ala Gln Leu Pro Gly

115	120	125	
Trp Asp Ala Gln Ala Val Thr Arg Arg Ala Leu Gly Glu Gln Pro Gln			
130	135	140	
Val Thr Glu Leu Leu Pro Phe Gly Arg Pro Gln Leu Ala Gly Gly Pro			
145	150	155	160
Leu Gly Ser Val Ala Lys Val Val Val Thr Ala Arg Ser Leu			
165	170		

(2) INFORMATION FOR SEQ ID NO:282:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 61 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:282:

Val Gly Val Val Gly Val Gly Ala Thr Ser Pro Ala Gly Ala Gly Ala			
1	5	10	15
Gly Ala Gly Ser Ala Gly Thr Gly Ala Gly Ala Gly Gly Ala Thr			
20	25	30	
Lys Gly Arg Ile Asp Ser Ala Ser Ala Leu Ala Ala Pro Leu Ser Thr			
35	40	45	
Gly Leu Leu Ala Val Pro Ser His Thr Thr Asn Gln Arg			
50	55	60	

(3) INFORMATION FOR SEQ ID NO:283:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 133 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:283:

Met Ala Asn Thr Gly Ser Leu Val Leu Leu Arg His Gly Glu Ser Asp			
1	5	10	15
Trp Asn Ala Leu Asn Leu Phe Thr Gly Trp Val Asp Val Gly Leu Thr			
20	25	30	
Asp Lys Gly Glu Ala Ala Glu Ala Val Arg Ser Gly Glu Leu Ile Ala Glu			
35	40	45	
His Asp Leu Leu Pro Asp Val Leu Tyr Thr Ser Leu Leu Arg Arg Ala			
50	55	60	
Ile Thr Thr Ala His Leu Ala Leu Asp Ser Ala Asp Arg Leu Trp Ile			
65	70	75	80
Pro Val Arg Arg Ser Trp Arg Leu Asn Glu Arg His Tyr Gly Ala Leu			
85	90	95	
Gln Gly Leu Asp Lys Ala Glu Thr Lys Ala Arg Tyr Gly Glu Glu Gln			
100	105	110	

Phe Met Ala Trp Arg Arg Ser Tyr Asp Thr Pro Pro Pro Pro Pro Ile Glu
 115 120 125
 Arg Gly Ser Gin Phe
 130

(2) INFORMATION FOR SEQ ID NO:284:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 63 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:284:

Pro Gly Ser Phe Ala Arg Thr Lys Pro Pro Gly Arg Thr Ala Asp Ala
 1 5 10 15
 Pro Ile Arg Cys Arg Asp Ser Arg Gly Thr Ala Gly His Arg Ala Leu
 20 25 30
 Asp Glu Pro Pro Pro Arg Gly Ser Glu Pro Ala Arg Arg Arg Ser Arg
 35 40 45
 Gly Val Arg Thr Val Val Val His Asp Ser Leu Ala Arg Arg Arg Val
 50 55 60

(2) INFORMATION FOR SEQ ID NO:285:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 72 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:285:

Gly His Gly Gly Gln Ser Ala Ile Gly Leu Gly Gly Gly Ala Gly Gly
 1 5 10 15
 Asp Gly Gly Gly Gly Ala Gly Gly Leu Trp Gly Thr Gly Gly
 20 25 30
 Ala Gly Gly His Gly Gly Ala Arg Arg Trp Tyr Arg Gly Pro Thr Ala
 35 40 45
 Ala Arg Ser Gly Arg His Gly Arg Arg Gly Trp Arg Arg Trp Ala Asp
 50 55 60
 Arg Gln Arg Arg Gly Arg Arg Arg
 65 70

(2) INFORMATION FOR SEQ ID NO:286:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 74 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:286:

Asp	Mis	Arg	Arg	Arg	Ser	Leu	Ala	Ser	Leu	Arg	Ser	Ala	Ser	Ser	Pro
1															18
Ala	Arg	Ile	Thr	Glu	Vai	Arg	Pro	Cys	Thr	Pro	Leu	Leu	Glu	Arg	Ser
															36
Ala	Pro	Gln	Ser	Gly	Ser	Arg	Asp	Pro	Phe	Arg	Pro	Trp	Pro	Ala	Asp
															45
Ala	Gly	His	Ala	Arg	Ser	Pro	Ala	Trp	Tyr	Arg	Leu	Gly	Ala	Gly	Asn
															55
Pro	Ile	Pro	Val	Arg	Ala	Ala	His	His	Glu						
															60
65															

(2) INFORMATION FOR SEQ ID NO:287:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 174 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:287:

TGGCAGCTAA	CACCGTGTAT	TGAGGGGAGC	CGCTGGCTAT	GGGCCGATTG	TATCCGTCGG		60
CGACGCTTTA	TTGAGCGGCC	GGAGGCCACT	CGGCTTCCAC	CAAGTGGTGA	CTCAGCGCGT		120
TTTCACCGCA	ACGAACGGCG	GACACACAC	TTGACATTCG	ACAGCACCGC	CGCG		180

(2) INFORMATION FOR SEQ ID NO:288:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 404 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:288:

TOGCCAACGG	GGTGACCTTC	CGTCGGGTTG	CGCTTGAQAG	TTTGTGCGAC	TTCGGCGTGA		60
CGTGGCGCC	GCACCCGACG	ACCGGTGAGC	TCACTCTCT	AGTGGAGGTG	CTGAGACGCG		120
CGCTGGGCG	GATGGGGCGG	GAAGGCTTGC	GCAGGGCGGT	GCTGGCTGTT	TTACAGCGCT		180
TGTCAGCGG	GTGGGATCGG	CGCTGGCGG	ACGTCUACAT	TCTGGTGAAC	GCGGAGCACG		240
ATGGGACCG	ACCGGGCTCG	CGGGATGTGA	CGACGTGCGG	ACCGCGCGTG	CATAACCGGT		300
TGGCGGAAAT	CGCTGGCGGA	CGGGTGTGCT	CGTGGCGGT	CGTGGCGCG	GATGGTCAGC		360
TGACGTACCG	GGAGCTGAGT	CGTGGCGGT	CGTGGCGCG	CGTGGCGCG	CACT		404

(2) INFORMATION FOR SEQ ID NO:289:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 134 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(iii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:289:

Ala Asn Gly Val Thr Phe Arg Pro Val Ala Leu Glu Ser Leu Ser His
 1 5 10 15
 Phe Pro Val Thr Val Ala Ala His Arg Ser Thr Gly Glu Leu Thr Leu
 20 25 30
 Leu Val Glu Val Leu Asp Gly Ala Leu Gly Thr Met Ala Pro Glu Ser
 35 40 45
 Leu Gly Arg Arg Val Leu Ala Val Leu Gln Arg Leu Val Ser Arg Trp
 50 55 60
 Asp Arg Pro Leu Arg Asp Val Asp Ile Leu Leu Asp Gly Glu His Asp
 65 70 75 80
 Pro Thr Ala Pro Gly Leu Pro Asp Val Thr Thr Ser Ala Pro Ala Val
 85 90 95
 His Thr Arg Phe Ala Glu Ile Ala Ala Ala Gln Pro Asp Ser Val Ala
 100 105 110
 Val Ser Trp Ala Asp Gly Gln Leu Thr Tyr Arg Glu Leu Asp Ala Leu
 115 120 125
 Ala Asp Arg Leu Ala Thr
 130

(2) INFORMATION FOR SEQ ID NO:290:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 526 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(iii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:290:

GCTTGTGAGCG CTACGAGTAC CTGTTCTCGG TGGGTUTOCG GGGGCCCTAC GACGACAAGG 50
 CCAAGAGAC CACCAAGGGC GTGGCCGGAGC TTGTCSCCTC GCGCCGGGTT AAATACTTGG 126
 TCTGCGGCG TGGGGAACAC TCGAACGGCG ACTCGGGCGG CCGCTCCGGC AACGAGTTTC 186
 TCTTCCAGCGA GCTGGCAACA CAGGGCTTTCG AGACCTGGA CGGTTTGTTC GAGGGTGTGG 246
 AGACCGCTGA CGCGCAAGATC GTTGTCACTT GCGCGCACTG CTTCACACCC ATCGGGCAAGG 306
 AATATCGGCA GCTGGGGCCC AACTACACCG TGCTGACCCA CACCCAGCTG CTCAATCGGT 366
 TGGTGGCGCA CAAGAGGCTG GTGCCGTTCA CTCCGGTTTCG TCAGGACATC ACCTGACCC 426
 ACCCGTCTCA CCTGGGTGCG CACAAACAAGG TCTCGGGAGC ACCACGGGAG CTGATCGTC 486
 CGCGGGGGCG CACCTGAGCG GAGATGGCGC GCCATCGCGA CGCGAG 526

(2) INFORMATION FOR SEQ ID NO:291:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 487 base pairs

- (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:291:

CTCGCGGCGCG	TGATCTGGCC	GGCGAACCTC	GTCAGTGCAT	CCAGACCCCA	ACGATCATCG	60
ATCAGGCGCA	TCGCGATGAT	CACCGACAGG	GCACCCAGCA	CCCGGGGGAT	GCAGGTTGAA	120
TAGAGGAAAC	CCCGGGTGAAG	TGGCGGAGGC	GGAGACGCC	CCCGACAAATG	180	
CCGAGGAAAC	TCGCGCAACCC	ACCCATCGCA	GGGGTAAGCG	TGACCGTGCAC	ATCTCGCTCC	240
CCGCGGTTAG	TCACCGCTCC	CAGGCGACTG	GCAGACATTC	GCACCGGACG	GTGCGAAAAA	300
TAGGTGATGA	TCGCGCCCGG	ACAGCGAACG	GCAGACATTC	GCACCGGACG	GACACCGGCG	360
CCGCGATAGG	ACAGGGCGAG	GCACCGCCCG	GCACATCGCT	GGACACCTCG	AGACCGTGCAC	420
AGACCGTACT	GCACCAACCT	GAAGAGCTGA	ACACTCCCG	AACCTGCAAC	AGCTGGCGAC	480
AATTGGG						487

(2) INFORMATION FOR SEQ ID NO:292:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 528 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:292:

ACGAAGCCG	AGATATGAG	CCGGGGCACAC	CGGGCTTATA	CGACGTTGAG	TTCCCGGGCG	60
CTGAGCTTC	GTGCTTGAC	GGCGCTGTC	CCTGTTGGT	GCAGGCTTTC	GAAGGTTTCT	120
CCGAGGCGG	CCATGCGATC	CGGGTGGCG	CCGGCGACCT	GAAGGGGGG	GTGGACACAG	180
AGCTGCTGC	GTGCTTGCAG	ATCGATGAAAC	TACTGGACTA	CCGCTCGCGG	CGGCCATTTA	240
TGACTTTCAA	GGCGTAACT	TTCACCGCTC	CGGATGATGC	TGAGCTAAACG	CTGATATGCGC	300
TGCGGGACAG	CATGGGKACC	CCATTGTTGG	TGCTGGCGG	TTTUGAGCGG	GACCTGAACT	360
GGGAGCGGTT	CATCAACCGG	GTGGGATTTC	TGGCGGAGG	CTGGGTGTA	CGGCAGAGCC	420
ATCGGGCTTC	GCACCCCTCC	GATGGCGGTT	CGCACACAC	GACCGATCAC	GATGACCGCT	480
CATTCACACA	ACGGGGAGGT	ATTCGCAATT	TTCAACCGTT	CGATGTCG		528

(3) INFORMATION FOR SEQ ID NO:293:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 610 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:293:

CCAGGCGCGT	CAAGGAGCCG	GTGGCGCGGT	TGCTCTGGT	GCGGCGGAGG	CGGGCGTTGC	60
CCGGCGTTGC	CCCGTTCGCG	CGGTGACCGG	GGTTTCTAC	CGTCGCGCGG	CCGGGCGAGA	120
TCGCGCTCGT	GTTCAGGGCG	TTTGGCGCGG	CCGGCGCGTC	ACCGCTTTG	CGCCCGATCG	180

CCCGCTTGGC	CCCGCTTGTG	GGGGTGGGGG	CTTGGTTGAC	GTATTGTTTC	ACCGGGCCCC	240
CCCTTGACCC	TTTGGCGGTG	TCGATGGCG	CTGCGATGGA	TCCGCGGACG	ACGACGCTGG	300
AAACCTCGCC	TGCCCGGCA	GGCGCCCAAC	TGTGTCGCG	CTCTTGCGAT	TGGGCCCCGG	360
CCGACAGAT	GATGGGCAAC	ACCGGAGCT	GGGGCCGCTT	GGGGGAGGCC	AACGCGGCGTT	420
CCGCGTCAGG	CCATACCCGA	CGGTGCGCG	CCGCTTGGGA	GATTTCGAGG	CTGGCGTGCAG	480
CCGATCGAG	CCACGCTGTC	CCAGGAGACT	GGGTTACGCC	GTGGCGCCCG	CGGTTTACAGC	540
GGGAGCGGCA	ATATGGCTGC	CCACTCGACC	CAACCGCGAC	TCCATRAGCG	ACACCATTCG	600
GGGTTGATGC						610

(2) INFORMATION FOR SEQ ID NO:294:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 164 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:294:

Phe	Asp	Gly	Tyr	Glu	Tyr	Leu	Phe	Tyr	Val	Gly	Cys	Ala	Gly	Ala	Tyr
1	5					10								15	
Asp	Asp	Lys	Ala	Lys	Lys	Thr	Thr	Lys	Ala	Val	Ala	Glu	Leu	Phe	Ala
						20			25					30	
Val	Ala	Gly	Val	Lys	Tyr	Leu	Val	Val	Gly	Ala	Gly	Glu	Thr	Cys	Asn
						35			40					45	
Gly	Asp	Ser	Ala	Arg	Arg	Ser	Gly	Asn	Glu	Phe	Leu	Phe	Gln	Gln	Leu
						50			55					60	
Ala	Gln	Gln	Ala	Val	Glu	Thr	Leu	Asp	Gly	Leu	Phe	Glu	Gly	Val	Glu
						65			70					75	
Thr	Val	Asp	Arg	Lys	Ile	Val	Val	Thr	Cys	Pro	His	Cys	Phe	Asn	Thr
						80			85					90	
Ile	Gly	Lys	Glu	Myr	Arg	Gln	Leu	Gly	Ala	Asn	Tyr	Thr	Val	Leu	His
						95			100					105	
His	Thr	Gln	Leu	Leu	Asn	Arg	Leu	Asp	Lys	Arg	Leu	Val	Pro		110
						115			120					125	
Val	Thr	Pro	Val	Ser	Gln	Asp	Ile	Thr	Tyr	His	Asp	Pro	Cys	Tyr	Leu
						130			135					140	
Gly	Arg	His	Asn	Lys	Val	Tyr	Glu	Ala	Pro	Arg	Glu	Leu	Ile	Gly	Ala
						145			150					155	
Ala	Gly	Ala	Thr												160

(2) INFORMATION FOR SEQ ID NO:295:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 161 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:295:

Arg Arg Arg Asp Leu Ala Gly Glu Leu Arg Gln Cys Ile Gln Thr Pro
 1 5 10 15
 Thr Ile Asp Gln Ala Asp Ala His Asp His Arg Thr Gly His Gln
 20 25 30
 His Arg Gly His Ala Gly Gly Ile Asp Glu Pro Pro Gly Glu Cys Arg
 35 40 45
 Lys Leu Gly Gly Lys Lys Asp Gly Ala Asp Asn Ala Gln Glu His Arg
 50 55 60
 Gln Pro Thr His Pro Arg Gly Arg Arg Asp Val His Ile Ser Leu Pro
 65 70 75 80
 Arg Val Gly Asp Gly Ser Gln Ala Thr Gly Gln His Pro His Arg Thr
 85 90 95
 Gly Arg Lys Ile Gly Asp Asp Arg Arg Gly Gln Pro Asp Gln Arg Lys
 100 105 110
 Leu Thr Gln Arg Asp Thr Gly Ala Ala Ile Gly Gln Gly Glu Gln Ala
 115 120 125
 Thr Gly Asn Ala Gly His Ile Ala Gly His Leu Glu Thr Val Leu His
 130 135 140
 Gln Pro Gln Glu Leu Asn Thr Arg Arg Thr Cys Asn Ser Cys Gln Gln
 145 150 155 160
 Leu

(2) INFORMATION FOR SEQ ID NO:296:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 175 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:296:

Glu Ala Arg Glu Tyr Glu Pro Gly Gln Pro Gly Met Tyr Glu Leu Glu
 1 5 10 15
 Phe Pro Ala Pro Gln Leu Ser Ser Ser Asp Gly Arg Gly Pro Val Leu
 20 25 30
 Val His Ala Leu Glu Gly Phe Ser Asp Ala Gly His Ala Ile Arg Leu
 35 40 45
 Ala Ala Ala His Leu Lys Ala Ala Leu Asp Thr Glu Leu Val Ala Ser
 50 55 60
 Phe Ala Ile Asp Glu Leu Leu Asp Tyr Arg Ser Arg Arg Pro Leu Met
 65 70 75 80
 Thr Phe Lys Thr Asp His Phe Thr His Ser Asp Asp Pro Glu Leu Ser
 85 90 95
 Leu Tyr Ala Leu Arg Asp Ser Ile Gly Thr Pro Phe Leu Leu Leu Ala
 100 105 110
 Gly Leu Glu Pro Asp Leu Lys Tyr Glu Arg Phe Ile Thr Ala Val Arg
 115 120 125
 Leu Leu Ala Glu Arg Leu Gly Val Arg Gln Asn His Arg Pro Gly His
 130 135 140
 Arg Pro Asp Gly Arg Ser Ala His Thr Thr Asp His Asp Asp Arg Ser

145 150 155 160
 Phe Gln Gln Pro Gly Ala Ile Ser Asp Phe Gln Pro Phe Asp Leu
 156 157 158 159

(2) INFORMATION FOR SEO ID NO. 337

4. SEQUENCE CHARACTERISTICS

- (A) LENGTH: 178 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(2.2) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:297:

(2) INFORMATION FOR SBC ID NO. 298:

SEQUENCE CHARACTERISTICS

- (A) LENGTH: 931 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

1142 MOLECULE TYPE: Genomic DNA

(4) SEQUENCE DESCRIPTION: SEQ ID NO:288.

AATTGCGAC GACGACGACG AACACCGCT TCTTCAACTC CGGGGACGTC AATACCGTA
TGTGCAACG CGGGGACGTC AACACCGCTC GGGGGACGTC GGGGGACGTC AATACCGTA

四〇

ATTTCAACCC	ANGCACTAC	CACAGCGGGA	CTGGAAACA	CCGGCGATT	TACACCGGCS	180
CTTTCATCTC	CGGCACTAC	ACCAACGGGT	CTTGTGGAGT	GGAAATATTC	AGGGCTCAT	240
GGTTGCACTT	GGGCTCTCGA	ATCCCTCGG	CCAATTCAAC	TCCTCNACAA	GCTTGCAGGC	300
GCACTCAGC	GGGGCTGAAAT	GATTOAATT	AAACGCTTAA	CAATACATAG	CATAACCCCT	360
TCGGGCTCT	AAACGGGCTCT	TGAAAGGTTT	TTGGCTGAAA	GGANGAACTA	TATCCGGATA	420
ACTGGCGTAN	TACGAAAAGC	CUCACCGCC	GCCTTCCTCA	CAGTTGCAGC	CCKGATGGC	480
AATGGACCTC	CCTTTTACCC	GSCATTAACT	CGGGGGGTGTG	GGKGTTACCC	CCACGTCAC	540
GCTACCCCTGC	CANNSSCCTT	RSGCCGTTCTT	TGCTTCTTC	CTTCCTTC	CCGGCTTC	600
GGTTCCGTC	AGETCTAAAT	CGGGGNNCCC	TTTGGGTTTC	CAATTATTCG	TTACAGSCCC	660
CCACCUCAA	AAATTTAATG	GTTAAAGTC	CTTTCGTTGGG	CNTCCGCTTA	WTNAANGTTT	720
TCGCCCTTNA	CTTGTGTTCC	CTTCVTTA	NTGAGMCTT	TTTCCACYGA	AAAMMNTCC	780
CGTTTYSGS	TTTCCCTTGA	WTIAIMGGR	AATTSCRATY	CGCGCTTGG	TTMAAATTA	840
CTTATTCNA	ATTTTCCG	TTTMMWATR	TTENSNCKGM	KNCTCCNREA	SSGNTTTCCT	900
GGCTCTTTS	GGTYYCCCRN	G				921

(2) INFORMATION FOR SEQ ID NO:299:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1082 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:299:

ATTCGGCAC	GAGATANGGG	CCACACGGG	TCGGCAGGCG	CCGGGACCT	CCCAAGCACK	60
ACCGGGCTCA	ACGACCAAC	GGTGGCTCC	AMGCAAGACG	CCGGGGTGT	GGCGGGCGAG	120
ACGGGCRACA	CCTCGCTTAG	CAGTCGGTGC	GACTCCGGGC	TCGCTGAAAC	CATGGGCGC	180
CGGCGCTCT	CGAACANGGC	TTCGCTTC	ACGCGTTAGC	CAGCAGCCAA	ACCGCAGCCA	240
GAACCCACAC	CGGGGCGGCT	CCGCGANAC	TCCGGCCAT	KCTGCGGGG	CGNATCCCG	300
CGATGCGTMA	CATGATGACT	GCTGCGGAA	GGCGGCGCT	GGCTCCGGC	AGCCCGCTGG	360
CGGGGGCAC	CGGGAACCCA	AGAACACCGC	RAAGGATATC	ANCCGAAACAG	CAATTGTCAA	420
GGGCTTAACAC	CTTCAGATCC	AGGGATTC	GGGGCGGAA	CGCTCGGMC	TGCAAGGCGA	480
CCCCCTTCTN	GGGGCGGNCAC	TGTCGAAAGA	TGCGATGAA	CAGKCTAGGT	CTTCGGCGA	540
TATGGAAAGN	GGCAACGGT	TTAAGGCGG	AAAAAAASTC	TGGCGATGGA	TTAAATCAGC	600
CGGGGACCCG	GGGTGACGKG	GGTTCGKG	ATTTTCAC	GGGTTTNAACG	GGCGTGCNG	660
CCCAACTTGC	GGGTGACGKG	GGTTCGKG	ATTTTCAC	GGGTTTNAACG	GGCGTGCNG	720
CGGAACTTAA	CGGAACTTAA	GGGTGACGKG	GGGTTTNAACG	GGGGGCHNT	GGGCGCTTAA	780
AAAACCGGNC	TTTTCTKGAT	TAMMAGCCG	GGGGGGGTTG	GGGGGCHNT	GGGGCGCTTAA	840
AMKCYCCCS	GGGGGGGTTG	GGGGGGGTTG	GGGGGGGTTG	GGGGGCHNT	GGGGGGGTTG	900
AAACCGGKYG	GGGTGCGTAA	WASSAMMCC	GGGGGGGTTG	GGGGGGGTTG	GGGGGGGTTG	960
CTTGGGAAAN	GGTTCGKG	GGGGGGGTTG	GGGGGGGTTG	GGGGGGGTTG	GGGGGGGTTG	1020
AMWTTNYCCNC	GGTTCGKG	GGGGGGGTTG	GGGGGGGTTG	GGGGGGGTTG	GGGGGGGTTG	1080
GGGTGNNANAN	AAASATTTTG	GGGGGGGTTG	GGGGGGGTTG	GGGGGGGTTG	GGGGGGGTTG	1140

(2) INFORMATION FOR SEQ ID NO:160:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 990 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(iii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:300:

AATTCGACAC	AGTGATGGCG	CTGAAGCTGG	TACGCGGGGT	GGCTCGGGTG	GTTCGGAAAC	60
RAAATCGCT	CGAAGTGGTC	TCGGTAAGCGG	GTGTCCTAAA	CGGGGGCGCG	GTGGCGGGGG	120
ATGATGATCG	CGGGCGCGTA	GTGCACTGCG	GGGGGGGTGT	GCAGTCGAT	GGCGGAATGC	180
TTGTTTGTG	GGTTTGTACCA	GGCGGAGAC	CGGTCGAGT	GCACCCGGCG	GGCCCTGATC	240
GACTCGAAC	GTTCGGGGAA	ATCGGGCGGG	TACTTGAAGG	TCTYGAACTG	GGCTTCAGAC	300
AACGGTTGTG	CTTGTGCGG	TCCGGGCGTG	AGTCGACATT	GGTGACACCG	AGTCGGCGCA	360
NCANCATATG	CACCGGTTTG	GAACCTATCC	ACAAACCCCG	TCCCGCTGTA	GTCACATTTGT	420
NCGGCGCTAA	TTTNTYGGCG	GGCAGGGGTT	TGGCGAYACN	KCCCGTGGCG	CAAAACTTCG	480
ANTCNCSSCA	AGGCNCNCAT	CCNCNCAAAC	AMGTTCACCG	ANAAAANATY	CAAGAGACAC	540
CTTCGGGKT	TTATTCATYC	CTTYYTGTGT	GGGGGGCCCG	CYTGTGDNAT	ACCGGTTGCA	600
AWTCCCAACN	CCCKCCAAJAA	RCYKGGGGCG	CCNCNCACCG	CGGGKGAAGA	WTAAATTAAA	660
CCCYAACHAN	ACTWMMWACC	CWNGGGGSCY	AAAMCUTYNN	AGGTTTGTCT	WAAGAGAASA	720
ANTCGGAAAC	CGGNTTACCC	AAARASACCC	CCNWTOCCCT	CRASATIGSC	NCGCGAAWES	780
AKGGCTCCNY	TCGCGNMMCC	CGGGGGGKKT	KGTTTACCC	WMRCKNMWYT	GGCCNASCNC	840
CKYVSSMMCC	CCCGCTCCCG	CTTCGKNTCC	CCAMCCYNNC	MGCGCCCCYT	GGKCCCCMEN	900
YNGCCCCCCC	AMMNNNGGGG	WGACCTCTGG	CCCGCRRHNG	TGGCGNANTGA	MCCTCNGHRA	960
MKCYCCNAR	ANMCCGNC	WGCGCERCRN				990

(2) INFORMATION FOR SEQ ID NO:301:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 223 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(iii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:301:

AATTCGGGTC	GCACCCGGGG	CCTGTTCCCG	AAACGGCGGGG	CGGGTGTGTC	GGGTGGGGCT	60
GGTGTGGG	CCGGCGCGCG	GGGGCGTAAAC	GGGGGGTGTGT	TGGGTGATGG	GGGGCGCTGGC	120
GGCGTGGT	GTGTGATGTC	GGCGGGGGGG	AAACGTCATA	GGCGCGGTCA	GGATGGGGGT	180
GGCTGGTTT	CGGGGTGCGA	GTACRGTCTGT	GGCGCGTGTG	CG		223

(2) INFORMATION FOR SEQ ID NO:302:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 418 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(iii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:302:

AATTCGGCAC	CAAGCGCGAA	CGGTGGCAGC	GGGGGCACT	CTGGTTGCCAC	CGGGGGGGCC	60
GGAAACCGG	CTGGCGGGGG	CCCGCGCGCC	GGGGGGGGC	TGATTCGGCAA	CGCGCGCAC	120
GGGGCGAGTG	CGCGGAATGGG	CGATGCGCTG	GGGGCGACCG	GGGTGCGGGG	CATCGTGGG	180
CTTGTGTTG	CTTGGTACGCG	CGCGAACCTG	CGGGCGACGA	CGAACCCGCT	GCACACGGCG	240

CAGGACAGGGC	CTTGCGCGCA	GTCAACAGGGC	CCATCGAGGC	CUTGACCGGG	CCCCCTGTAT	300
CGGCAACGGG	CCPACCGGGC	CCGGGGCAAC	GGGGCCCCGG	GCRCGACGGC	CGGCGTGTG	360
TTCCGCGGGC	GAAGGAACGG	CGGOTCCGGC	GTCAANCRCG	GGGGCGGCGG	AAATGCGG	418

(2) INFORMATION FOR SEQ ID NO:303:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1049 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:303:

AATTCCGAC	GAGGGCGACG	ATCGCATAC	GGCTGCGGCG	CAGACCGGGC	CGATACGCGA	60
GTCTCGACAA	CGCGACCGCA	CAATACGGCG	CTCGTGTGTC	CGCTTCGAC	ACGACCTGCT	120
TACCGCCAC	CGCGGGGGCG	ACCGAGTCGG	ACACCGTAAAG	CCTCATGGGG	TAGTTCACG	180
CGGAGATCAC	CGCCACGACG	CGCTCGGTT	GATAGCACAC	CGTGTGCTTG	CCCATGCGGG	240
CGGAGACGGG	CTGTCGCTTA	CGGGCTTTCA	CGGGTCAAC	ACAGACTCTT	GGTTTAAAT	300
TCGCCTTCCG	CGGATCAGAT	CGGAAATTTC	CTTTGCGGG	GGCCATGGGG	CTTGGCGCG	360
CTCGCTTCTG	AGGAAACTCG	TCGAGGTCG	GGGTTCTG	ATNAACAGGT	CGGGATACCG	420
CGCGATGACT	GCAGCTGCGA	CGATACGGG	ACCTTGGCG	GTGCGTCTG	CCCGCGCGAN	480
CTTCGCGGAA	TCGCGCTTGC	ACTTGGGGCG	GGGGTCCGAC	GGATGTATTA	CACGGGTTTC	540
CGGTTTAAAC	TCTTCATAT	TCGGTGTGAA	ATTCGGACAC	TCCTTATGTC	GGCAAGTCCC	600
AACGAAACAA	ACGGCGCGAA	GGTTAGGTT	YAAAAATTC	GGGTTTTCG	660	
CMAATTTCG	CGKRNATGKG	TCGCGGTT	GGGTCGTC	GGGTCGTC	NTGNGKGGAK	720
CCAAAMGGG	TGGGGGAGG	GGNNNNCAAN	CTTWCACCG	TKTAANGGNN	TCGCCCCCG	780
GGGAKKKGGA	ATTCGCGGAA	GGCGGGGGG	GGNCARATTG	TYCCGGMCTC	CTCGGGGAWTC	840
WGGGTTTCG	CGAAAACGCA	GGCAATTTG	TTTCGCGC	CTTGAGACN	CTTTTAKRCA	900
MMCGSSAARNS	AMMCNCTTCG	CGCTTGTTCT	AAAAGGAAV	CGGCGAAATT	TTTANTTSSC	960
CGGCGGGGCG	CGCGCTGTTT	TCGGMTWU	WVNTGCKMCC	MMMSNCKSNG	KGKGNRCCNN	1020
CGCGGCGGCG	AAWYNTGCGT	NTATAGAGC				1049

(2) INFORMATION FOR SEQ ID NO:304:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1036 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:304:

AATTCCGAC	GAGGGATAC	AGAAATCCCGG	AATGGTGAAAG	CTCGTGTGCG	TGCGCGTTACG	60
CCAGAGCTCA	GGGTCACGCG	CGGCGCGGTC	GGAACTCTGA	GGCCGACCGG	GGAAAGGGTG	120
AGGGCTGGGG	TGGGATTAACG	GAANGTACT	GGGATGGAAA	ACCGGTTATTG	CATATGTTATT	180
GGGGCGATGGG	AAATGGGGAA	GGCTGAGGGC	GGCTGTGTTG	ATTTGGGGAA	TTTGTGTTGAA	240
TTTGTGTTGAA	CGAGACGGGG	CGAGCGGCG	GATGTTGTTG	TTGGAAATTG	GTGCGCGCGA	300
CGGGTGTGAT	GGATGTTGATT	TTATGGGGCC	ATATGAAATA	TTGGGATGTC	CGACGGCGAA	360
CGGAGATGGG	GGGACGTTCA	GGGGCGGGAC	AACCGWAGGT	CGGAGTAAK	GGTTGCGTTC	420
ATTTGGGGAA	GGATTGTTGCA	GGGGCGGGAC	CGGAGTAAK	GGTTGCGTTC	NAACGCGCG	480

TTTATTTGCG GCTTAYGGGA ATBAMRGAA CAAINTCCCT CCGMGGAAA ACCAACMSSC	540
CCTGGTNSYC CCCCCRCNC AKAACCCRTT KCTGTGTTNC CCGMAAATNA CCCCCSCTS	600
WACTCCNCG AANTNSCCCCC CCGCCNNNTS ATSTYCCCGK GTTCCCGCMC CCGTTTAAAC	660
TCGCGGTTT ACGCCCGWNT SNCNCGGGCS YTAALMMCRG GCTTSTTNTCT CCGCCYTRMK	720
CCGCCCTCK SAMCNCNC CTCXGAGAC GCGCKYKGSN TNCCCAATNT MCNACCKCNS	780
KTINTMCTK CCAATTCNC CCGCTTCCC CCGSTSTCAM WTATAAAACC MCNYAYWYNN	840
KNCHMARTA MIGACNTCTNY NCCCNCCNCK NTITKAMWQC CCKMCCCKSW TWCYCKCSCC	900
CCMTCINNAC YCCCGGCKTNT NKGMCCTCC CCGCCCTCCCG MCNBBMETCT YCGSGKTNWC	960
NCNTTNTTCN CYNAMMCKK KTCCTTCCN CCGTCTCGG CCGWCGCCCV KKCICTSKCC	1020
CCNCTCCGSC MMKGSC	1080

(2) INFORMATION FOR SEQ ID NO:305:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1036 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:305:

ATTCGGCAC GAGATCATGA ATAGCCTGCTG GGTGAGCACC GAAAGTGTGTC GCGGATCTGC	60
GAGCAGTCT CCGCTGCTCG CCCAGCAGGA GGTGCGCATC GATCGGAGCA GCGCGGATG	120
CTTGAGATGT GTTCAGTGC AGGTAGGCC GACGCGCGAG CTTTGCTAGC AGGGTGTGTT	180
GGCTTCTGC ACCTGAGGA AGCTTATACG CCGAGGAGCA GAAATCGGGG GCGTGGATCC	240
GGGTACGAG CTCGGGGGGG GCGACCGTTC GTCGGCGCTG GCGCGAAGGT CAGCTGCTGT	300
GCGATCGAG TAAGAACCCG CCGCATCGG GTCGGCGAATG AGCACTGACC GAGGAAACGA	360
ACGATCCTCG TCCCTTCTG GGGGTAAATC GAACTCGAGA ATCGCACGAG CGACCAATCA	420
TTGGGAACTCG GCGACTGACG GACCAACCGG CTGTCGAGCA CCGGAGGGA ATTGGTGTG	480
TTGGGCGGCG CCGGNAACGG AATCAGCGG AGCGGCTCGG CGAASCANCE GCGTANACNT	540
ACATANCAAC GCGTTCTTC CGCGATTTG GGGGTGTTGC CGTTCGCA CCGNAAYNC	600
CGCGATTTCG AGCGAAAGAA TTGGYCCATY ARNGTYCTCTC CCGAAAACCN ATTCGCGCTA	660
TCGCGGCGGGG GGGGCCCCY MMGAAAAACG CGGNAANCC CGGGGGCGCC CGGGGTRWNT	720
CGCGTTGCG CGCCNCSSG TTTGGTCTCM CGGCGMMTNNW CGGNTGCGCC CGCNCNAAAA	780
AAAAAATCGNG AGCAATTAAGA CGCGYCNAAAG ASKTTGGGSSC CGGACCGGCG GCGKAKIWA	840
ANTTTAACCC KAAAAGAAAGM CGGNNMCCCC MGGGNCTTA AGKTTTADG GTTSTTNNNG	900
AGAAAATMTC GATATATNSK TTNNAAAMAA ASCCGWAKCC CGCGNNKNNN CGAAWKAARK	960
GGCTTGTGGG GCGWGGGGG KKKKNTNCM KMMNNNTNGR CGCGCCGCTN NNTWKGCTTM	1020
TCGNGGNGC GNCAGN	1080

(3) INFORMATION FOR SEQ ID NO:306:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1060 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:306:

ATTCGGCAC GACTGCGATTC GATCGAACAC CGCGGCGCT CGCGAGGGCA CGTGGCGAG	60
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GGCATGGCCA ACGGCTTACTG GGCCAAACCGG AATGCCATTG GCGTCTCACCC GCAACCCCCG 120
 AAACCGGGGA CGCGCGCATG GATCAACCGG GCGACCCCCG ATGCCAAATA GCGTCCACAT 180
 AATGAGACAC TGGCGCAAAAG AGCTTGACAG GCGGGCGACCC ACGCRAAGCTG TTAGACGTGT 240
 CGGTCTTGCA AGAACGGGGT TGGCCACCCG AGATCACGCC GCGCGAGGGC ATCGACTCAA 300
 CGTTGGCGGT GTACCGCGCT AACGTCGGCG CGGCCAAGAA ATGACGGTGC GCAATTACCAT 360
 GCGCGCTGCTG ATCGACCTTG GCGACCTCGG CACCAAAACT ATGANCACCC TTATGCCGAG 420
 TCTCGTGGAC ATCGCGCAACG GCTTCAAAAA CTGCTTGTGG ACAAATGGTAT TGTGACGCC 480
 CGCAATTCTT KTCCTTGCAAA GAACACTCA TGTTCGCGGT AAACAAACCTY GOTTINGAAAAA 540
 ACACGCCATA TGAAGTCCC ATTCGGGCAAGA GAAACCGTTCG CGGAAGGTGT TGGGACGCC 600
 TGTGCGGCCAA AAATCCCGG NGGTTAAAMM CGCNSNATGG MSAATTTCG CTINGACRAM 660
 AAAAGGCTCA AGKYCAAAAG NGCCUCCCCG SONAAATTGG TGAACCSAKA WYANRTTCCC 720
 WWWTNCAAAT KTTNGGTTGC KNTTCCCTNT AAANGGCGCN CCCCNCRRGG GMGTTTCCC 780
 NNNNMGGGGN CYYCSCCCCA AAAAANAMM KTTTCGKGGG SMGGEKCCCC CGCGGTYNGG 840
 GKYTTAACG CGCGKGGGTT CAAAAANAMM ACACCCCAAMS NGGGGGGAAA ATTTGAAWT 900
 AAGGKKEKTCG SCHACCCCA AAANNNNNCCH ANHCCCGMK SARGGGGGRY TIMKAGGOMO 960
 GNYCCCCCWW YCGGGRGGHNA AAAYAAACK NGNGMGGAT NTNTTTTGTG RSSSRNKT 1020
 TTYTGTCTYCN CGCMGNRWWG SRAMNTGTS HSSGGGSGCC 1080

(2) INFORMATION FOR SEQ ID NO:307:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1040 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:307:

AAITCGCGAC GAGCTTCAAC AAAGAGCTGA CATTGGCGGT GATUCCGACAT CGCATCGGG 60
 GCAATACGGG CATTGATGAA CGGAAGGANG TCTGGGCTTC GCTCAACTGG ATTACGGTTG 120
 CGTGGTGTGAA AGCGTTTGGG CGGAAGAATG CGACCTTCACTTGGCGCTTC CACCGTGCAAA 180
 TGTGTTGATG GATGCTGGAA CGCGCTCTGAG NGATAAAGAA TTGGCTGGTC CGCGGGCAGH 240
 ATGGATGTCG CXTTGTTCG TCCCGCGTCA AATTCGCTGTG GATCATCTG CGAGGTATD 300
 TCCCGCTCTG AGCTCGAGCC ATGATGGATG TGGCGCTAAC GAAAAGTTC TGACATCGG 360
 CAAGCGATTC CGGCATCTGC CGCGCGATTT CGCAACCTTCG TTGTGTTGAA CGGTMTCAAC 420
 CGAAATCGGG GCTTAAAGAC NGCTCTGGGT TGATTTAAC CNAACCCCTN CNAATYCTTG 480
 CGGNGNMGTTG CGCTTCTTCG NACTGGCTGGG BYTGCGCGCG TGAACCCNA CTNCCCCCCC 540
 GTTGGACTTA MRTNTTCAAA AACCGGTTTA ACACGGAAATTN SAACCTTCGG TCAAATRMM 600
 SAATGCGGC TTYYGGGNNCC CGCGGAAAW TTCHNCNNGG GMNNTYCTCN CGTTTGGGCG 660
 SAAAATTTG CGTNCYMMN TTACGAGGC NEMTNTMTG CGGECNNNAAS GNGCCCGGGKK 720
 TTTTTNCAAAT TCGCGGGGGGG GGCYGRFTMC NGGGGCCCCC CGGCCUKNAA 780
 AAAAANCMGA ERCCNCYGGG KKCCCGCCCG NNATNGGCGC YKRAAAACAA ACCCCAAARRA 840
 TNGNOMGGC SMACISGWK GYNAAGGGGT TSNSCTMANN KKGMAANNCT SGMSCCNNNN 900
 NCTGMGGKTT TTKKNGNARL AAANAMMGGG RCGGGHGGCNM GAAAGGGMS GSCKSCNNNM 960
 NGASNGNWNCG CRNNGANRCC NGNGYGNMNN NNNGNNGNNN CGGGRNNAACN NMEMCANSMC 1020
 HNNMGNNNN CGYMTNKCGC 1080

(2) INFORMATION FOR SEQ ID NO:308:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 348 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(II) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:308:

AATTGGCAC GAGACAANGG CTCGAAATGG GATCCGGGG AGCTGGGGCC CTCGCTCAC	60
GACCTTGTG CCAACTCGG GCGCGGTT CGCGTCATG GGGCTTAGTT ATCTGGCGCG	120
AGCGTAACT CAGGGGAGA TTTCGGGCTT TTTCGCGCC TGGCTCACG TTGGGGGAG	180
TKGGGAGCG CGAGGTTTG CAAACCGGA CGGGATCTG GCGCTCGGTC CAGGACTGTT	240
ATTCGTATA CTTCGATACA TGTGACCAA CTGTGNCNA TATTCGGGGC GCTGCTGTC	300
ATTCGCTTC CGCGCGTAA GTCCTCAC TCCCTTTTC TCCTGCGG	348

(2) INFORMATION FOR SEQ ID NO:309:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 332 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:309:

AATTGGCAC GAGAGACGGG GTCGTTGACG AACGGACGCT TGGGGGGGGG CGCTTTCGCT	60
GGCATCAAGCT CTTCCTCTTC TTACCGCTT AACGGCTGGG TCCCTTGTG CGTTTCTGGA	120
CACCGTGGT ATTCAGCGAA CGCGGAGATA TCTTGAGCG CACACCGGC AGGTGCTTC	180
CGCGGGGGG CGCGACGAGC ACCATCGAAT GCTCTCTGAG GTTGTGGCCC TCGCCGGGA	240
TATACCGCT GACCTGAGAC TGACTGCTA CTTCACGGGG CGAACCTTCG GAAGCGCGA	300
ATTCGCTTC TTGCGAGTGG TGGCTCTGCG CG	332

(2) INFORMATION FOR SEQ ID NO:310:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 942 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:310:

AATTGGCAC TACTCGGTTT AGACGUGATT AATGCTCCG CGAGCACCTC CGACTGAC	60
ACCTGCGG AAAATGTTGT CAACTGTGTT AACGAGCCCT TCCAGACGCT CACGGGGCGC	120
CGCGTGTATCG CGACCGGGCG CAACGGGACT CTGGACCGCT GGCTTGACGC CGGGCGCGCG	180
GTTGGCTTT CGGCAACGGG GCGAACGGGG GTGCGGGGGG GAAAGGGACCC AACGGCGGGG	240
ACGTGGGAG CGCGGGGGGGG GCAATTCTTCG CGACCGGGCG ACGGGGGGGG CGGGGGGGGT	300
CGACACAGG CGACGGGGGGG GACCGCGCGC CGCTGGGGG GCTTCTGAT CGGTCTCGGC	360
GTTGACGGG CGCGGGGGGG CGCGCTGGG CGCGGGGGGG CGCGTGTACCC	420
CGATGTTTCTT CGCGCGGGGG GAAAGGGGGG GCGGGGGGGG ACATTAKACG CGCGCGACCC	480
CGGGGCGGGG CGGAAAGGGG GGGTTTTTCC AACGGGGGGGG CGCGGGACCC GNGGGGTGTT	540
CGTTTGGGGG AGGGCGGAACT CGCGCTTACG TTAATGGGGG ANGGKTCAGC CTSATGNC	600
MTTAAAGGAA CGTTCGCGGTTT CGCTGGAAAGA ASRWNKNGT KGGCAAAACNA	660

SNNTCTTNN	WATTKGKGNNA	AAAANCCTT	CCWCGRACT	NCCTCCCGNM	GRGMCNNTNN	720
NTTTCGNCNN	CCCGGSNAAM	ATNTTATTTC	NGGGGKNTCN	GGGTTKMNNA	AACCCCAAM	780
MRNNSKCSA	ANGGGKNSGC	NKNNMMNSGT	TTTCGKMTA	MENWTYKNN	NTCNGARSNN	840
NAAMCNGNK	NGKCKNNKAA	AEENNNTWTKT	KNSCNCNN	GRNGVREGG	CKNGGSNNNG	900
MCWNSNARNG	NGDGSNCNC	SNEDNAAAA	AASGQVNC	NSMKNKKEKG	NRGGGGGGGG	960
GG						962

(2) INFORMATION FOR SEQ ID NO:311:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 323 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:311:

AATTGCGAAC	RAGAAGACGC	CGGAAGNTT	GGCTGCGCTT	TACAAGTCTA	TCAARGGCCA	60
GGGGGAAAGC	AACTTGGGCA	AGATCTAGT	TGCTTCTCCC	GAAGCGGTCT	CGATGCCCA	120
GTACCTCGC	GCACCGAACG	GGAGCTQAC	CGACGATCCG	GGCGGAAAC	GGCTTGGTT	180
GCAGAGAATG	TGGTGGAGG	TGGCTTGGAG	GATTGTCAN	GGGACGGCNG	TGACCGGGAC	240
GGTTTGGTGT	TGCTGACTC	TGCTCACCAU	CGCGGCGAC	GGTTGACCT	CGACCGCTG	300
CACCACTGTT	GGCGCTGTG	CGG				323

(2) INFORMATION FOR SEQ ID NO:312:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1034 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:312:

AATTGCGAGT	GTGTTGCGG	GGCTCGAGA	AAAGATGAT	GGAAACATCG	CGAGCGCCCG	60
CCAGGTTATG	GTGGGGTGA	TGGCGAACCA	GGGATGATE	ACCGGACATAC	ACCGGGCGCG	120
CCCACCCCC	GTGACTTCT	GTGACTGAGC	TGCTTTHAGC	CAAAGCCTGT	AGACRAACAC	180
ATAAAACGCG	ACGTTGACCA	GGGGCGACAG	CCCGGCGAG	AGGTTTCTGG	CGACCATATG	240
CCAGAAGAAC	GAGATCACCG	TCAACTCTAC	CGGAGTGGCA	ACCGGTTTCC	GGTGGGCACC	300
GTTCCCGGG	CCAAAGGGCG	GGCGGCGGT	CGCTTCATCA	CGGTTGAT	ATGGGGCGTG	360
GCNACCAAGT	GAGCGTTGTT	GGCCCGCGCG	CGGTCATCA	CGGCGGCG	ANCCTGTTGA	420
GCATGANCAG	CGGATGAAATG	GGCCCGCGCG	TGTTGCGGT	CGTGCCTGAT	TGACTCTCT	480
CNACAACTTG	GGGGCGCACT	GGAAACCGGG	TGAATGANTG	AATTTCRAACC	GTSAAACANT	540
AACTCATATA	CGCTGGGGGG	CTCTTAAACCG	GTYYTGAAANG	GGTTTTTTCG	TTAAAGGAAG	600
AACYATTTC	GGATANAKTGG	CGTTNWTAAC	GAAGAGCCC	CGCCCGATNGC	CTCCACAGT	660
TTCGCGCTGA	ATGGGAAATGG	KGNCNCYKIR	CGGGGNNTTT	AAACRCGGCG	GGTTTTTGT	720
CGCCNCCTGA	CTTGGMMTGTG	AKKNCNCYKIR	CGGGGNNTTT	AAACRCGGCG	GGTTTTTGT	780
TWNGKTCGC	CNNAMMNTNN	ACCGGGGGCC	SKCCCTTACG	TTTGGCTTC	NTCCCCCNST	840
MAAANASAAAN	GGGCKRNGTV	CGTTTGGCNC	CGGACGATCG	TWTKTTTGG	GGCCGNCDC	900
CGNTKGGNN	CTGTCNCNC	GAARAMAMCC	KCCCCGNTS	TTTGGTVAAG	GTNRKNCMSY	960
CGCGGGGGY	MNINNAAYAAN	MMNATNCNN	STRANMAKCN	NNNNNNNNSCN	MNINGNNTCN	1020

SCNSNNGGEBG CSCC

1034

(2) INFORMATION FOR SEQ ID NO:313:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 331 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xii) SEQUENCE DESCRIPTION: SEQ ID NO:313:

AATTCCGGCAC	GAAGGCCACAT	CCGGGGCGCG	TCTTTCGATG	ACTCGTTGGT	CATCGTCGAC	60
RAAGGCCAGT	CTCTGGACGCG	CAATGTTGTTG	CIGACCTTNGC	TCTCCCGGTT	GGGGACCGGCT	120
TCCCGGTTGC	TGTTGACCCA	CGACATGCC	CAGCGCGAC	ACTTCCGGGT	CGCGCGTCAC	180
GAATGGTCCC	CGCGTATGCA	CGAAAGCTCA	AAAGTCTTCA	GTGTTCCGC	CACATGCGCT	240
TGCTGGCGCA	TGAGCGGTGG	CGGATGCGCG	CGCTGTCAC	GAGATGCTCG	ANGAGATCAC	300
CGGGCCCGCG	TGAGTGGCCC	TGCGCGAC	A			331

(2) INFORMATION FOR SEQ ID NO:314:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1026 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xii) SEQUENCE DESCRIPTION: SEQ ID NO:314:

AATTCCGGCAC	GAAGATCTCA	CCCTGGCAGAC	CGTGTGACGCC	AGGCCACGCC	ACCACTTACG	60
CTCTGGCGC	CAAGATGTTG	ACCGAGCTTC	GGCGATCGCG	CCACACCGAC	TGCAAGCTGAG	120
CACCGGGATC	GGGGTCTCTCA	CTCTAGGGCGA	TRAGCTGGT	TTCCGGCATCA	CGCGCTGACTA	180
TGACCCCGCG	TGCGAAAATGC	AGCAAGCTGGT	CAACGGTATC	GAATCTGGGT	TGCGCGCTCT	240
GGTGGGCGTC	ANCGACAACTT	CGCTGCTCT	GTITACLAAGG	ATCGGGCTAA	GCCTTCATCC	300
CGGGCACTCC	CTACGGCGCTC	CGGGCGGGGG	CGGGCGCTTC	TGCGGACGCC	CGGAGCGCT	360
CACTGACGCC	ATCTCCGTCG	CGCTTAAACCC	CGTGAGAAAGG	TGGTGTGCG	GCAAGTTGGG	420
CGCGCGTCCC	CTGTCGACCC	CGCGCGCG	CGCGATGCTG	TTCGACACCA	CTTSGNGACNC	480
CGGGCAAGGA	CTGTCGCGGC	AMTNCAGGAA	NTTCGTGCG	GCACCGCTT	CTTCGCGTGT	540
CTGTCGCGGC	ATGTCGCGGC	AMTNCAGGAA	NTTCGTGCG	GCACCGCTT	CTTCGCGTGT	600
GGCTTAAACT	TCCTNATTTT	CGCGCGGGCT	CTGGCGTTTC	GCCTGGCGCC	NTCTTNGCAA	660
ATGCGGAAAG	ATCCCGAACMC	AAACCCCCCG	GGTCTTGTGGG	GCSCGGGGGG	GGCCNAWNCC	720
AAACCTTCCCC	TTTAAANTGT	TTGKTCGCG	CGCCGGCGCC	GCNAANSCAH	CGCTTTEGGC	780
CTGTCGCGGC	CCCAWTTAA	CGGAKCGCC	AAYCCCAAGY	TTMGGCCCYC	KNAAAAAAA	840
ATTTGGCGCG	CCCCAANTAA	ATTCGCGNGC	CCYTTGGGGG	GRANCYNT	TTTMCCGSSS	900
CGGGNNNAAMC	GGGAAACCGGG	KAAYTMMTCG	NAAYCGCCSN	RAMBNNTTTC	TAANNCGCC	960
YNGCCCGAAA	ATTNNAMAAAM	UMNNKTCGNG	GGGGKTTTNC	EGKXGRAGGM	AAAANNNEN	1020
CGTNNMCNNN	SAMNNCNNSNN	SGGNNSNNNN	NNNCNCGYKG	CSNAANMCCC	CGCGGGGGGG	1026

(2) INFORMATION FOR SEQ ID NO:315:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 324 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:316:

AATTCCGGAC	GAGAAGAGCG	CGGAGATST	GGCGTGGCT	TACACTTCA	TCAGGCGCA	60
GGGGGAGCG	AACCTTGCGA	AGATCTACGT	TGGCTTCCC	GAAGCGGTCT	CGATGCGCA	120
GTACCTCGGC	GCACCGCACG	GGGAGCTGAC	CCAGGATCG	GGCGCGAAC	GGCTTGCTT	180
GCAGAGATG	TGGCTTGGAG	TGGCTTGGAG	GATTTTGCAG	GGGACCCGCG	TAACCGGAC	240
GGGTTTGTG	TCCGCTACGC	TCTCTACAC	CCGCGGACCC	GGGTGACCG	TGAGGACACT	300
GCACCACTCG	TGGCGCTTGT	GGCG				324

(2) INFORMATION FOR SEQ ID NO:316:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1010 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:316:

AATTCCGGAC	GAGGCGTGGC	GCTNAACACT	AGCCCCUOOGC	TGCGGAGATAT	CCCGGACTCG	60
GTAGTGGCGC	GGTGGCGCTC	GGTGCTTCTTC	GGACGGGGCG	CGGGCGACAT	AAGGTGGCTG	120
ATGCCCAAGT	ACGGCGCCCG	GTGCGTGGG	TGATGATGAG	TGGGACTCTC	CGCTGCGCG	180
ACCGGGAGGT	TGGGATGGG	CTTGATGACG	CAGGACGCGT	AGGACAAAGTC	GATGGGATGC	240
ATAGTGGGCT	TGAGATGCG	CTGGGATTCG	CGGGGTCGTC	CGGGCGAAAT	GGTTGGATT	300
CTACTGGCG	TGGTGTGTC	CGGGGATTCG	CGGGGATGAT	GGGAAACCGA	GGATGGGAC	360
GAACGGGTCT	TGATCTACGT	TTGGCTTCTTC	GGGACGAGCT	GTGAGACANCC	GGTACTTGGC	420
ATATATATGG	GGCGAACTCG	GGGGCGACCG	GGGGCGACAT	AAANACGGGG	ACAGACATCG	480
GGGGCGCGGT	CAACGCAACG	ACANCTTGGC	ATGGGATTTC	GTGCGCAGCG	CTGAAMCCGT	540
CGGAGACGCC	TGTGGGGCG	GGCTTGGTAA	GGGGTTGGT	CCCTGGGNGCA	600	
WTAAATGGAA	AAACCTTGGC	GGCTTGGTAA	GGGGTTGGT	GGGGTTCGGK	CCCTGGGNGCA	660
AATTTTTCG	GANTCGGTG	GGGGGTTGG	GGGGGTTGG	GGGGTTCGGK	CCCTGGGNGCA	720
AGGTTTTCTT	GGTGGGGGG	GGGGGTTGG	GGGGGTTGG	GGGGTTCGGK	CCCTGGGNGCA	780
MNAASCONTC	CCCTTTTACG	GGGGGTTGG	GGGGGTTGG	GGGGTTCGGK	CCCTGGGNGCA	840
GGCCCGGMAG	CGGGGGGTG	GGGGGTTGG	GGGGGTTGG	GGGGTTCGGK	CCCTGGGNGCA	900
CGGAAATTTC	TTGTCGCG	GGGGGTTGG	GGGGGTTGG	GGGGTTCGGK	CCCTGGGNGCA	960
MMRAAATTCG	GGGGCGGGGA	GGGGGTTGG	GGGGGTTGG	GGGGTTCGGK	CCCTGGGNGCA	1010

(2) INFORMATION FOR SEQ ID NO:317:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1010 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:317:

ATTTGGCCAC GAGGCTGCC GCINAAACACC AGCCCCGGCGC TCCCCAGATAI CGCGGACTCG 50
 TTAGTGGCGC CGGTGGCGTC GTTGCTCTCC TGACGGGGCG CGCGGACCATN AAGGTCGCTM 120
 ATGCCCAAGGT AGCGGGCCCG AGTGCATGGAG TGTATGATGA TGCGACTCTC CAGCTCGCG 180
 ACCGGGAGCT TGGCATGGG CCGTATGAGC CAGACGGCGT AGGACAAGTC GATGCGATGC 240
 ATATGGGGCT CGAGAGTGGC CGGGCANTTC CNGGCTGCTC CACGGCAAAAT GCCTTGGATT 300
 CTACTTCCGC TANTGTGCC GCATGGCTG CGGGATGAAT GGGAAACCGCA SGTGGCGAC 360
 GAACGGCTT GANCTCAAGT TTGGCGCTTT CGCGAACAGTG GTGNACANCC GGTAACTCGCC 420
 ATANATCTGG CCNAAATGCG CGCGCGGCG CGCCCACTN AANAACGGGC ACNACACATCG 480
 CGGCCCGGT CACCCNAACA ACANCTTGGC ATCGGATTTC GTGCCCGCGC CTCAACCGT 540
 CGCGAACGGC TENTGGCGG NACTCTTCTT MNATAWAACTG CGCGCTTCCCGC CGCTGGNGCA 600
 WTAATGGGA AACCTTGCN CGACCTTGA NATTTTTACT GGTAAACCCC 660
 AATTTTCCG GANTTGGCTG KGCGGGGTTT YSTTTTCCCC ACCTTGNAN GGGCGCGCCA 720
 AGTTTCTT SYTGGAGGGG GAAACCCCAAC TTINITYTYY AACCSOMNAA NYMITYTCG 780
 MNAAACCCNTT CGGGTAAAGT CAMGGSGGTN AAGCAGTTTG NGKITAALAAA CGGSGGKNTG 840
 NCCTCYMANG GGGGGGAAAAA TSTETCNGG CGGGCGAAAM ACMMMHYGN GTGKGGKRS 900
 CGSAATTTT NMWMAACTN GGGGGCGSSGA MNTTTNAAG MCCCCCSNNN GTGKGCGGNN 960
 NTTTCCNNAW MMKKGKNNNNN SNMNSCENGCG GKYNSGGSNNN NHAAGMGGG 1010

(i) INFORMATION FOR SEQ ID NO:318:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1092 base pairs
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:318:

KGNGGGGNGN NTICAYCAYCA YCAGCGGGYH UNATTGGGG CGCACTTGTG MAASAGATTT 50
 CGAAYTGGC AMGAGGCGAAT CTGTGCGNCCT GTCTGTCGAAN CCAATRAGGC CTRAGATG 120
 CCATCTCCACA AAAAACCGTTT GTGTGTATYNT SCCRCAATR AAGGCGCGCG TINTACWC 180
 CGCGGTTTCTT CCGATTCGGG TKTGTGATCT GCCTGGGGTTSR AAAYCCCCCG TTTTGGAYCC 240
 CGCGGATTGAA ACTGGCGGTG TGAATGACTCC GGTGTTGGCGA TCGGGKWWTT GAMSTCRCG 300
 ATTAAAAAAAC CGGGTGTGTT GTCTGGCGTC CCAAATTCG AYCCRATAYT CGATGGCTG 360
 KTGCTVTCCK YCGGTACCCA ARYCTGGGTA TCTCTTACTG GYCCCTTAAGK GCAANWYCKEG 420
 JCTGTYCIMT TTGGCGGGGT CCAAAATGCA CACCGCGGT TCTTTCCTATA CCAAAACCGG 480
 CTGGGCGCCK AGCGCGGAAAT AAAKAKATAT RAXAAKKGTCG CTNHYCCAAA AGCNCGGGNN 540
 CGCNANTNNC ATCCGNTNNC MSCNDDCCCA CGCGTGAAGK TKSGGAAAYTT CTNMAACCC 600
 CAANACCCA TAACCTTGCN GAASAAACCC CTYCGCGGGG GYCNWNCAAA ACASCTTAT 660
 TTGCTKSTT CGGGMWCGT GCGCGENAAA YCCCAJAATTA GTTTTTCGGGT CGNAGAKAAA 720
 ACCNCGGGNN CGCCCGCSNAA NWATATYTTT KGCGCAANCC CSAAACCTT TCGNACCNCK 780
 ATTTMCCTT CGCGVSCAAT TGGYCGGAT NOGGNCCTY TTAAAKKKSC GAGWNNNGNG 840
 GRRNNAGCNA AGCGCGAAGT CGMNAAATN CGCGGCGCTC CNAACACGNN TYTTCGSAAA 900
 ABCCWCCCCC CGCCCGTCAA AACTCCCGNA RKANTHCCCA AAAACWYNGS GCGCCCCCCC 960
 CAAACMAAA AMCCCGGCGN NMCCCCSKKK KTTTTCTT TNCOMRSOCC 1020
 AAMGCMWY KSKTOMAAAAG GGAAGCAGNC TYCCSANANM TCCCGNWSH CGCGSGMOMNA 1080
 GAALSMCCCCC CS 1092

(i) INFORMATION FOR SEQ ID NO:319:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1251 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:319:

GGGGGGGGNNN	NATACATCT	CYGTGTYACCG	GGGTTCTAAT	GGCGGGCGGC	AATCTTGTC	60
ASAGATCTCT	NAMTTTCGGG	ACAAAACATW	GACAAASATYNT	CGGGCGNMTTC	GTGTCCTNNKA	120
TCGCAAAACG	NOTRACASAC	ASACATCTAT	GTGTTGGCCCG	CASCACTYCK	TTGGGACCTC	180
GCTTACCGGG	TGCGGCGG	OCACCGTGC	GTGCTATCC	RACCGCGGCC	ACGGGGGGGG	240
ATATTCAGG	CACCACTG	AGTTGGTGTG	ACATACGCTT	GGCACTTTCG	TCTAANTTGT	300
TGAAACCGGA	TTCTGTTGGA	ACCCNCCGAA	CCCCNCCN	AACATTTGGG	NTCCCGCGTT	360
CTTCCCGACG	CTTCTGGGGG	GTTCGCGGAA	AANCGACCCG	WGGGWTCTT	TCGCCCGACG	420
GGCGGACAA	NTCGGTTGTT	ATTTTGTGCA	AYCGGGCGCG	GGATCCGCGA	ACGGGTTGCG	480
GAATGTTT	TCAGAACCGG	GGAKCCGGA	TTTCGGGCG	ANAAAATTCN	TCNCACCACT	540
GCTTCTACTT	CCCGGACCGG	AACMANTTC	ATCGCTTINN	GTCTGCGCTT	GGGGCGACGG	600
CTAAAYACCG	CTTTGGGTT	CGCAACCTGC	GGGCCAANTG	CCNAMCGRGA	CTTTCNATTG	660
GNTTCGATT	GGCCCCCGGT	RAMACCGGCC	NTGGCCENNT	CGGAASSAAA	NGGGGCGCTNT	720
KGGCNCBCCC	AGTAAANACCG	TACCNMAYTS	CANTTTTTCG	CAAATTTNGG	ACAAANSKTG	780
GNTTTCGGGK	ATTTTYYTTS	GGCNCCCTG	TATGGGSPFTN	GGGGCKCYNC	NCSTKIGKCA	840
NAASAKAYCCT	NGNNRGGGGT	ACCCCGCTTG	GGGGGTTTTT	NGSGCCCGCC	AWAYGNKSTG	900
GGCCGGTCHNG	GGAAKATWT	MWWTMCNCGG	GGGAATTTT	NTSTCGAMCS	SGGACYCCCR	960
GGGGGGTCTT	TCGGGCGGSA	NNAWANGGGG	GGGGGNAAXT	NTQNSQNGGGS	KNMTTATTG	1020
TTTTCGCTT	TKACMSGGG	GTTTKRAONG	GGGGGAAAGAA	ANAAAAAAA	RAKGGYENTT	1080
TKYMCACNCT	GENNNWANR	NAAGAGCTCT	CKKNCNCNCB	NTTTTCTTTT	MGSNSDYGUGG	1140
GGNGNNMARA	ACKHSZEMMAC	KCSYTCCTCG	NCMGGGGGGS	NGSGCNSTYN	1200	
GGNGKGRNTA	TNTNGENCTN	SCCTCNCGCC	GGCGKNTGTC	TMTCTNMGYGG	1260	

S1 INFORMATION FOR SEQ ID NO:320

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1099 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:320:

AAYTCGGCAC	MGAGTATTCAC	CAKCTGTYGT	GGCTGCGA	AUTGGAGCTA	TTAATACCTG	60
TTGTGATCC	TCRACATCT	CTTCGCGTAC	TTGGGTGGGT	GGATGGTGGC	CTGCGTGGAK	120
TCRAAGGTCT	TCGCGCAAGC	GCTGATCGCG	CAAACCTTTC	GGCCGACAC	ATCAGCGCC	180
AACACCTGAC	CTGCGCGGCS	ACCGGGGGYC	GTCAACTRACT	CCAACACCGT	GGCMTGCTG	240
CTGGCCNACY	CGGTGTCGCA	ANTGAACTTC	ASCCGCGNMA	CCAJMAACNA	NAACCGTGT	300
CTGAAGGCCA	GTTCGAAAAAC	CTGAAGTWC	GGCCCRCTT	CCCGAAACGG	TNGGAGTCKA	360
TCGAGAGGCG	GGGGGGGGGG	TCAGACCGGT	TGTGGGTTG	TCAGGAGGTC	TCAGGAGGTC	420
TCGCGGGMTC	CGGGTGGCTCA	GGGGGGGCA	TTTMCAGGGG	GGGGCGCNAT	CAAATTCGGG	480
GGGAGACGG	CGCGCGCTCNK	GGAGACCGCC	TGCGGAAACG	CYCGAACGGK	ATCCCTTCKGK	540
NAACNCGCGA	RCNCGCGKX	TCCGGGCTTC	NMSGCGAATA	CCCGNMCNIT	CGGAATCCAA	600
TTGCGGMYGG	CTTTTYYTCC	GGGGGGCGCC	AAAYNGGGYC	CTTASNSNMK	KNCCAMANT	660

CCNNTATCTGG NGCTCCCNAN KYKGGCGTTTC	NMAATASAMIA	MMNRGGGTTT	TSCYACMMN	720
AACCGGDNKG KCCCOMKCTK MAMAAAKATT	RATCAGKNGG	GGKCKKCNCH	NAAMACCSNN	780
CNCGNCWYTC TMYCSSLONGC GCSMYNANCA	SNNGGGAGGW	GGSGRMEMCT	CIMTGTCTCT	840
NGCGCCNNTN TYCKSGAKAT ACASNMKCTC	GGCNGCGCH	MAAMANRAIA	CTAKCGYGN	900
CCSNSTTIVN CTSNMMNHN TCCOMWNNAKNT	NTTYGKCNNA	KCTMKATKNC	CCCTSKCNKX	960
MRAMTCCTYQ SNMTCCTCGA TCTCTCKKSC	SNMSKHTCKC	RSCHNCNCHNN	CNKNMCKNN	1020
GGNSTRCCY TCTMNNNTCS AGCKCGSKNC	WACNCACACK	NGWCTTYFTCC	WENNMKCNKX	1080
TOKCKKACRG MTMTCWCCS				1099

(2) INFORMATION FOR SEQ ID NO:321:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 296 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:321:

GGNGTATACA TCACTTGTGVA CCSAGGATCW ANTGGGGCGC	MAAKCTNSTM	CASAGATCTC	60	
AAAYTCTCGA MGAGUCGAC	AKAKITCTGT	CCMRAKCGNG	CAYACWCCNG	120
CTTGTACCGG GGCKATGCGA	ACGCTTGCG	GGCGGCGCGA	CCACGCGCGC	180
AGCGGCCCGN TRAMCRAACC	ACCGCGCKTT	TACGCCCCCGC	GCGGCGGGGG	240
CCCCACCGGC ACCACCCUGG	CGCGCGTTGC	CAAAACAGGC	CCACCGTTGC	300

(2) INFORMATION FOR SEQ ID NO:322:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1073 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:322:

NGNGISGNKMY ATCATCWTTG	TGCAACGNNG	MTCAATTGCG	GGCGCAATGT	TSTMNAGAGA	60
TCTCGAAYTO GGCAGGACCA	TCIGCGCGG	GAATGTCGAA	AWGTCWTTAA	CGGOMATCGG	120
TTTCCCGCYCA CTKTGTCTCA	SKCATGCGG	GGCAGNWTYC	AACRATTAT	TIGGGYCGAG	180
AAAATTTTCG CTKTGTACSA	ACCTCGAGG	GGTCAASCAA	CGACGCTCTRA	ACCCTAATY	240
CTKTAGGTNKT YCGGCGAACG	ASCYCRATAA	TSCUGCCCGC	AMCCACAAAA	CCTGANTNGT	300
TTTTGCGRAA AGCGGTTGCG	GRAGGGGTGA	ACTCGCTGAA	GGTNTTCWYC	NCCTTTRACAT	360
TAACACCCCG CGGTTCTWCG	CGCGCGCGCA	ATYCYTCCG	WTKGCHACCA	YCCCANCTG	420
CGTGTAGGTT RAANCASTSG	SGRAACGCGM	MCCSTACCKC	TOGCTGTATYC	KGCGGNTCCG	480
SKAATTGCGG GATTTACCGG	CGAGGTTAA	CGAGGCGCC	TMTGCGTCKY	CGACIAACCGG	540
ATCMMWNCNN CGACCTTCTTA	AATTCCTTGT	GGTGGAAACCG	AMYCGAAAAA	NMINTTYCCG	600
TCCGMMGGGG CYCGGAAKKT	CHACNTGQNT	WACCGCTCKC	YTTCGAASSTT	TCTGNCGCCG	660
GGCCCKAAAS ANACCGGAAAC	CGCGGAAYTS	WTAGGCGTCT	TCGCGCGTTA	AACTKCNWCYC	720
AATCCCKCAA CGCTCCCGCG	GTTGCGTCT	TAAMTTGCG	CGCKSCASNG	GAATYCYKSG	780
CGCGTGTATW CGCGCGTTT	CTYGGKNAAC	SGCCCGCNGW	GSCTVCCCCN	SNTRSSGCCS	840
GTTGGGAMYC AAAAHTNGGG	MMCNTRAGCGC	SGNACGCGCN	GKGGGGSATW	TKAAAYTCGG	900
GGGGGTGTC	CCGTC2CSNAA	AAGYGTGKQG	ECGCGSCCGYC	CGMARTTTT	960

ACCAAGGAGG CTCGGCCTINCW WGGCTCCCSN SNSMAMAAAAN NKCKCCKGGG CKGARRNMNA 1020
MCTCGNGG WTCGCKKTC HSCNSGNCGS YGCGSASWCN KNYCNCACACA ANC 1073

(2) INFORMATION FOR SEQ ID NO:323:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1166 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:323:

GGCCCGGCGT TMMMMTTCAY TATTCACCGG GGMTCAGTG CGGCCGCAAK CTTTGTCAAC 60
GATTCGAAAT TCGGCGAGS AACATSTGCG GTCRGGCGAT GTCRGGGTGGG GCAACTTGG 110
GCTCGGAAAT YCGGGGTTG CGCGCGGTTG GATGGGTTG GGTAAATATCG GGTGGGTTAA 160
TGGCGGAGC TCAATTGCG GTTGGGCAAA ATATGGGTTG GGCGCAATATN GGGTCGCTA 210
ACACCGGCGA TGGGAAATTTCG GGTATTGGGT NACCGGTTGAA AAYCTGACCGG GGTNGGTG 260
TTCGAATACG GGTAAACGGGA ATGTTGGTGT VVYACCGGG GSACCGGNNM VTTNGKTCGT 310
TMMNCNGTSC CGKSAAATNS KNGGTTTSC MTCGCGGGA TMTTNNMCC CGGNAKCKSC 360
WAGGCGCTGT CATYCCMCMG SGSSGCGTCA MNCCACCGTG NGYVCCCTCG MNMTGCGAT 410
GNTGCGCTGTG CGTNTTMGNC CSCNCGYCTG AMGNCYTKSGK CACGNTMNG CGACKGTTGT 460
MCYMCSCAJEN MTGCGGCTG CGTTCGTTG MCMCSCTCTM TCAAACTCKC CGGGYCKNC 510
MYCTTCGKCC AYMAACCKX TTYCVCNWCWV YMCKECKAG WYKNCNCCTC ACTCTMNTTC 560
TGTGCGTCKC CGAACCGTGT CGTCGCGGCG CGACAKAYMG YANGMNTTSC MTCGAKLSCC 610
CIVYCNKNCM NMNCNCTMCWV TNNAKCAGEN TGTGCGTGTG MMFTTMACKL WNNNTNCCK 660
SGACCGTGTG ACTGCKCNCG TGTGCGTGTG CGYMCCKTG MNKNCGCGTG MMTCMTCXAT 710
CGTCNCGNBY GYYYAKAAGC MNGTCCCGAN KMCAGCTCTG CGGCCAKGMS ACINCKCCCG 760
CGTCGCGATG MCTGCGCTGT ATCTCGTCTG CGYMCCKTG ACNCKCCTGATT CNACTMNNWN 810
CGAACGCTGT CGTTCGTTG ACYCTGCGK CGTMCCKGMC NGWCTTGTCTG CGKCGCNCRN 860
CGMMNCNGM CGTGGCGMNG YTCGCGGCGT CGTMMKCTGTG WNGCNGTCCGT CGKCGYVNT 910
CGTCGCGTGT CGTTCGTTG MCTGCGCTGT CGTMMKCTGTG WNGCNGTCCGT CGKCGYVNT 960
ACCTCTCTCG CGKCGCNCRN CGTTCGTTG 1010
1140
1186

(2) INFORMATION FOR SEQ ID NO:324:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1230 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:324:

NGGGGNNNNT CWTACATCWN TGTINACCGG NGMTCTWATT CGGGCGCGAW NGTTTGNMNS 60
AGAATCTCN AAYTCGGCAC AATGATCTT TSTMTAKTGT GCGGGGGNGC CACGGCGTAT 110
GTCGGCGCTGG GYTRACCGAA CGCCCGGCGS CGGGCGGCRAC AGGCGGGGTA TSCAGGGCGC 160
GGCGGGCGG CGCGYTTATG RAAGGCGCGV TTTCGTCRATG AGCGTSCCGC CGGGCGGTRA 210
TTACCGGCGA RAYCGGKNTT TGGGTTTATG AACGCTTAATG GCAACCGWTT TTTTCGGGT 260
AAAAACCGCG CGGCGCGATG CGGGCGGNGT TGGGCGGATG YNGGCGAAAAA WTNTGGCGC 310
AAAGGCGCTT TGGGCGGATG TGGGCGGATG CGGGCGGTTG GCAAAACGTY CGGGCGGTTA 360

TCCGKTCGCG	GGGCGCGCCN	AAAACCAC	AAATYCGGTYG	GGGGTGKTYCC	CMCAGGCGGT	480
TGCTYCGGTY	CAACTCGCCA	AAAYYCCCA	ATKATTGGTG	SCYCKTSGGG	FTSYTGGGTY	540
CAATTACCCC	CNCGGGNAAA	GRAAAANAAA	ATCNCCTGTT	TCCTCGGTYA	YCTTTCMTTGG	600
3AAAAGGGC	ATGGGCGGT	TTTTTACCT	CAACCCCGA	MCATNTWACT	YTCGCGCCQG	668
GGGGCNAAA	C3GTTNGCTC	CGGGGNAACCC	TKGITMCCCG	ATCNAAAAGGC	CNGAATTTGG	720
TTTGGTYCNA	ATTWTTWXXX	CCCCWCGTNG	VAASAAKCCCA	AAASAKCCCK	YCNCAAMMVK	780
NGGGGTYTSG	GGCGKNCCTK	GGGTTTAAAC	CYCCCCAAA	YNNSGGGKET	TCGGCYNBAT	840
KCCACCCNCK	GGGGGGGUN	EEAAAAYAY	TTTCCCSAAA	ATCCGACCVY	TCVYKTSSTRY	900
AMACACCCCT	TYUUKKAYTO	CKYKSCNATTC	SGMITCMAAA	TYCOSYGGCT	TTTTCGCCCC	960
CGGGCGCCG	AAWTGTTGK	INCNANTTYC	CGGNAAMMCH	AWTGGGGES	KCCATTCCTGG	1020
SCYTMAANTA	AAAANAGGG	KKTTTYYCTY	MANAAACACH	GTGKCNNCN	CNAJAAAASN	1080
AAKAAAAGAG	KKEMTNTNSA	AACCCNCCCC	CTSTTYTINYET	TKTNNMNCKCC	CYGGKIGKGM	1140
SWSWYNTTGT	NGGCRCCCC	YNNKNTGANA	AAAMMNCYCCS	GGSTMCRNAM	ASNNMNTTCK	1200
STSTNGGCC	ICMBAANANAM	MCAMWKWYCC				1230

(2) INFORMATION FOR SEQ ID NO:325:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1022 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:325:

NGGGGGGKNA	TNAUCWCTC	ACSSGCGTC	TGGGGCGGAW	CTTGTGMAASA	GATCTCNAAY	60
TGGGCGGNN	SCATATTCMC	CATATTAACG	CATTGGCGTC	GYWTGCAWCT	CAAAWCTYTC	120
CTTGCGKCGG	TTTGTACRAAG	GTGGGWTGTY	GTWTYCCTRAA	SCCGTCTRATV	TCXTXTATYC	180
CTKGCGCTC	ACTTTAACGG	BATGCGTCC	TTTGTAVGATT	BATGCGAATTA	WTGGYGRANT	240
TTTGTGAGGG	RAACGGGCTY	TTTYCGGCGA	GRACAAATGA	TGGGAMYCGC	TYCGCRAGGC	300
CGGGCNCAC	ACCGGGCGNN	AAAGGGYCCCG	CGAAWTSCCT	GGTGTCAAAGA	TGGTSCALAC	360
AAAMCNATCC	GGGGYTTAAC	CGGAGYTAMC	ACAAGAAAAT	TCGGWTGGCC	GCACCAANNT	420
TTTGTATGTY	CWYGGGCCCC	TTAACCTTG	YTGGCGTATT	GGCTKCTCTGC	CTCRACAGCM	480
YNGGCGGTT	AAACTTGCGGT	GACTCGAATC	GTGTGTGGCG	AMGGGGGGYT	CNCMGGACAA	540
AAACCGGTTA	TTGGCGGTTA	TCGGCGGCGC	TCGGGGAAAN	GTGTGATMTTC	TCGNAACCSA	600
CGGGGMBTTW	TAACCGTQAA	CGGGSGNKG	MYNSCGCGGA	ANTTTTCCT	TYNGGGCGRN	660
AAACGTTT	AAAGTGACCC	KUGGGGGGCG	CCCGYTTGGG	AAAACAACCC	CKATGGKTT	720
TGAAAATTTT	TKNCGCCCCA	TTTGSGGGGG	GGGGCCCCACG	CCMCTTITTC	TCMSCHMITY	780
TCYVGGGAAT	TTVTCGCGCG	GAAYYCGGGG	CCXCGCGTAA	MCCECMNNWGG	GYVSTGNEAS	840
KGATNAWT	TCSTTYYMC	CGGCGNNCC	CCCGAAGCCT	KNTGTAACMA	AAAKCGGGGG	900
GCNNMYYWY	YCNNGNKT	TNGGGSSNTT	TYMAAANMAN	JGGGKYWTTY	CKCCGCGCN	960
GXTTGGGGST	TTTCGNTTTS	GGGSSATYKG	MACCGGCKMT	AYCCGCGGGGT	NTTKTKYCCCG	1020
SC						1022

(2) INFORMATION FOR SEQ ID NO:326:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1081 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:326:

NCAGGNNNTTA TAAAGCAGGCTT TCAATTGCGG CGCCACATCTT SINAASAGAT 60
 CTGAAATGCG SCAGAGAAGC CAGCTTATTTG KGTGRASCSC ACCAGCUGA CCTCGCGKT 120
 CKTTTCTTC AGRGAGGCGC TGGGTGGCRC CGTGTGCGAT GCGACCGCC CCCAAGAACN 180
 CGCAAAHTY CAAAAACAA CCAGGCGGTTA GTCGCGGGCG GCGAAAGAAA TAACGGTCTT 240
 AACCGAGGC ACAGGCGAACG GSYCCCGGCCA AGTCAGCGNA CCTCCCGCC NATAAGGCG 300
 GTGGGGGCTT CKTATYKCC AATGCTGCA TGTAGACGGG CGGTCGCGWT TCGCGCTCAT 360
 CGCTCTTC TIMMATTTC GTCGACAGY CGGGGGAGCY TTTCAGCNC CCTTGGCGAN 420
 CACGAGGAGG CAAAAATTCG CGTGGCGTG ENKAAGYGR GATTGGGGTY CGKETTTNT 480
 TGTGCGGAGC CGCCGTTTCA CGCCGTTTCA CGTGTGATCC CGCGGCGCGG RGGTGTGAA 540
 AAATGCGGCC AGATTCGAA MTCCTGGCC TTTCAGCNC YVCCTTCCG CGCCGCGAA 600
 GGGCGCGCY TOGGGAGNT TCGCGGAAAA AGTCAGCGCC TTCGCGCGCA AGAAAGTCG 660
 SACTCTTCA TTGGGGGAG ATANATAATTTT YCKTNGGGCG TTCGCGCGCA AGAAAGTCG 720
 RGGGGAGAAC AGGTTGTTTCG AYYGGGGAGC MTTTCYCCYEGG RGGTGGGGCTT TAAAGAAGC 780
 SAACCCGGGG CGYCGNCGGCG TACGGCGGAAK AAAAATTCG CGGCGTTTCG TYYNNKGGG 840
 CGCCCGCGAC ACTTGTGTTT TCGCGCGAA MTCCTGGCC KOMMAMMIG KNGCTTTTT 900
 YCSCGATAMA CTGGGGCGCT TGTGAGGGCG CAAAGAAGG CGCGGTTCTG TTCGCGCGCA 960
 YTGCGGGAGA AGAAAGAAGT AAGGTTAAGGG TTKCGCGCGCA CGCGGTTCTG TKGCGCGCA 1020
 CGGGGGGGGG CGTCTCGCGC CGCCCGCGCG CGKAGATCGG CGCCGCGCGG NCAGGTTTCTG 1080
 CCC 1683

(xii) INFORMATION FOR SEQ ID NO:327:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1069 BASE PAIRS
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: SINGLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: GENOMIC DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:327:

GGGGNNKTYT MCAYCWTTC YACGGGGGNC TATTCGGCGC SCAGTGGTCA GAGAGATCTC 60
 GATGTTGCGA MGAAAAGAGW GAGTGCTGCG ACCTTTCMCGC GCGGGAGCGC ACCRACAAAG 120
 RAACCGCGCC ANAATATGG CGCACATTCG TCAATATCTT ACCAACATTT ATYAGGGGATT 180
 MCATTCGCG GGACCRACCG CAACTACCGC ATATCTGTTT GCAACCCCTT ACCGGTCCCA 240
 MTTGCGCGCA STTGCGCGAC GCGGAAAGAA CGCGCGCGAA CGGGCGCGCA MTCCTGGCTC 300
 CGCGCGATCA CTAGGGCGAT TKAAGGAAAC CGGGGGCGC NANTTGGCGA ACAGGTGCTC 360
 ACAGGGGGC CGGAGTGGGG CGGGTGGCGW TTTCGACNCCC TTTCTCTCGA CGGAATYGG 420
 TTCCGATTCG CGWGGGGCTT TKGCKKXTC KGGGGTCCCA ATTCGCGGTA TCTCTATRKG 480
 TCCCTAAAT SCNAATCTG GCGYCCATTG MTCGGGTTTC NTTTGGMMAS SRGGGTTCT 540
 TTCTTTCGCA ACCGGTGGG GCGGNNMCGA AAAAATGATN ATAATAATGK YSCCTTCAA 600
 ACCCGGGCCC CCATTCGCGT CGGGTTCCAG CGCGCGCGGT TAAAGTGGGA ATTTTNNNN 660
 YCNAGCGCTT NTTTGGGA AAAACCCYCG GGGYCTCAA CGYTTTTTTT GSNSSNNTGG 720
 GCTGTTTCCG CAAACCGCA ATTTTGTGGG GGYCGCTCAA AGCGGGYCGC RCGGGAAATT 780
 TTCTTGGTC AACCTTAAACG TTTCGACSCC TTTCGCGGTTT TCGCGCGCMM TNGGGGGNT 840
 KSSCCNTTCY RAKKCGCGCGG GGGGGCGYCM CGCCRMNTTC CTTTTCTTTT CGGGGGGGAA 900
 NGKTTCTTC AAGMCGCGCC CGCGCGCGAA AGCGCGCTTAA GTTTTCGCGA RGGNNTGGN 960
 KNCCCCCCCCC KGGAAAAGAT YCSCGCGGAG ACMSMGGGAA CGCCCGGGGGN TTGGTTTTT 1020
 TKGCGGGYCCG CSMASYYTTT TKAGMAMAKA TKGCGCGCGCA TKGCGCGCGA 1083

(xii) INFORMATION FOR SEQ ID NO:328:

SEQUENCE CHARACTERISTICS

- (A) LENGTH: 1210 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(4) MOLECULAR TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:328:

NGGCGGGKMK	ATACATCTT	TCTTCACGSSG	GGATCATTG	CGGGCGGSC	TCTGTTGCAAA	60
SAGATCTTGA	TTCGCGGCT	MMACCCCGAC	TCCAAAAGAA	ACCRCAAWCT	CGGGCGGCTCY	120
RAAAGTCTTG	GGCGCGKTC	AATTTAACAC	ATTCTGTC	ANAGTCATC	CGGCTTACGT	180
YCCCGGCAAM	GGGGCCACAA	CCTOCAGRGA	SCACYCRAAT	GKTVYTGKTS	CGGGCGGCGG	240
CGGCGTAAAG	GGACCTTSCG	GGGTTCGSC	TNCACAAATG	NYCGCGGAT	YGGCTTGTAT	300
MHCAGCGGG	GTCAAAAGG	CCGACCAAGG	CACSCACCC	NTTACGCGGS	CTTAAAGANGA	360
AAAAGGGCTG	ATGCCCCGAA	GGGGGCCGCG	CCCCAACCTT	CGTGTGTC	ACGACCCGGT	420
CTCTCTGCGG	ATGGCTTCTT	GGGATCTTCTT	CTGTCCTCT	TCGKTYCTCT	CGGATACCAA	480
ATGGGGTATG	CTATATACTG	GGCGGAAWTT	CGAACATGTS	GCTGCGGCTT	TCTGTTGCGT	540
TCGAAATTTC	CGCAGAACCG	TTTCCTTNGAT	NCACAAAACC	GRTKGGKCC	NRACCCRAAA	600
AAATGTAATG	TTATAAAGGG	KGKTTTTCAC	ACACCCCGGG	CGCGATTCGA	TYSGNTTCC	660
MMGGCCCGGG	GGGGTAGGGT	GGGAAANYCG	TGACCGYVCA	ACCCCTTWS	TTTNGRAAT	720
KAAACCGTTC	TCNGGGTCW	TYMAAAAMA	NTTATTTGGG	NGNTTTCGGG	MNNCKXRENST	780
SCCGAAATTC	MAAATATTC	TTTGTGTCMA	TTTAAAMCG	YGCNCNCNC	GGAAALAAATT	840
TTTGTGTTCA	GGGCCCCAAC	TTTTCGTTGAA	NCSSKTTTGT	CTTCCCCCCC	AMNGTGGGYS	900
GGGGATKGGY	TCYTTCTTCA	TKTGTGTTW	CGGGGGGGG	KGKTCMCCCG	CGTTTTCYCY	960
NYWTTTGTG	CCCCCTTMA	MMRAAANGG	YTCSYNNAAA	AGGCCCCCCC	SCCCTTCCCA	1020
RAAANCCG	MMRRAAANTT	TTMKKNNNN	SCCKENKNGY	YCCCCCCC	YMMRNNAAAAAA	1080
AATMYCNC	RASANMCA	MMGGGRNRS	CCCCCCCCSTT	MMNNNTTMTTNT	TTTTTCTCRA	1140
GGGGCGGCGS	MMHAMMEN	CTTTTTCGNC	NNNNNNNNNN	GGGGMNCCK	CCNAGAAMMW	1200
CGGGATGCG						1210

INFORMATION FOR INC 100-129

3.1. SEQUENCE CHARACTERISTICS

- (A) LENGTH: 1105 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANGENESS: single
 - (D) TOPOLOGY: linear

MOLECULAR EVOL. OF HUMAN DNA

(2) SEQUENCE DESCRIPTION: SEQ ID NO:339:

NGSEENNGKA	TMCATCWCYT	GWACGGGOMT	GTATTGCGUC	CCGAACTGCT	MAASAGATUT	60
CGAAATTCGG	AAKANACACCE	ACCGCCGTTST	MTATACAGCG	CAAATGTTCT	GTGTTSCCAAA	120
ACGGGAGACGT	GGCGGCCGCGG	GGYTTCACAC	GCKTTCATYR	ACCGGGAGAG	TCAGTGTGTTA	180
ACGGGTTTGT	RAAGGGGCCA	KGCAACCTAA	ACGTTTTCAC	CAAGRANTYG	GTGCGGCCGC	240
AGGGACTTGT	TGTGGTTCG	CTGCGCCTGTC	GTAGGCGCGG	TIANCGCGG	TTGGCGTGT	300
AMCASCSCG	CONTRATRAT	AKINWTTTCCG	GGGCGGCCAG	CAUCGGGAC	TTTGGCGTGT	360
GGCGGCCAATT	CAAACYKTCYT	GGTTCTCCCG	AAACACCAAC	AAAGGCCAAC	TTTGGCGTGT	420
ATMGGGRACT	TTAAGGCCCA	GGCAAAACCT	NTRAKCNGCT	CGCGGGKRAA	GTCGCGGCAA	480
SCRATCMAA	AAAKACCTAA	TTGCGCCASC	AKCACCACAA	MMCCSETTTC	TCTTCGCGA	540
TTGGGCGGAA	TTTTCGGGCT	GGGGGGGGAA	AAACGTTCTT	MMTCATGCGG	GGCGCGCGAA	600

ATTTGCGRAA	AAACCCCTRY	CCCCGGTTTT	YCTTGCTCMG	GGCCAAANACC	CCCCGGAAATC	660
AAAAAAGGTC	GGNCAANGG	GCMAAACCCS	SACCCMACTT	WTTCRERTTN	GGGGGGSCNN	720
CCGAGTTAA	AWKSCCTCY	CTSSCCAAAY	TGGKONAAA	NNGRKTGKG	TTGGCNAC	780
TTTTCGGK	CCGGGKGEGG	WKGYCTTMMMA	CTTTTNTTTT	CCCCYKAAA	NYSCCCCCCC	840
CGGSSCCCCS	CCGGGGGGGA	NTTTTTTAMA	GKKTVCDDCT	CCCCAMAAA	ANACCCCNYC	900
CCSGGSCCT	ITKRNAAAMN	KTSCCCCG	GNNGGGGKCM	GKTTATTTT	NNNCSCCDDC	960
TCGGCOSAA	AAATAKMTT	SYVCCCCMC	CTCGKNCNG	GHAMMSMCSC	TCGGYCTCNC	1020
GCNKGTTAAM	RSNCCKRNN	CONCYKCGS	NSNGKONWCD	NCCGTSSNCT	NYGCNCNCNC	1080
KAAAANAYNC	NGGMSSTSSMN	CNKCC				1140

(2) INFORMATION FOR SEQ ID NO:330:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 936 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:330:

NGENENKRN	TAMAYCWWYC	TSCACSGNGA	ACWANTGCGG	CDRMAWCNTN	IMKASAGATO	60
TMGAAYTGGG	CGAAGGGCGC	AGAGTGTGTT	GCATCTGGTC	ANAGTSTTMA	CGCGTGCDDC	120
CGGGTCKGTR	GASCACMCT	HTGCGACAC	CAACCCXTC	GGGGYCAC	GGCKTCGCGT	180
GCRAAWYCC	CCAGGCTTAC	TCAACBAY	YCTTCTGCA	CUCARGCCT	TYGGCUCGCC	240
RATCCTGKKT	CASYCOCCK	TGCGTGTCCC	RAAKTACTG	CCGAYCAAA	CCGCTCGCGG	300
RAACRAACTT	AAATYTGCGG	AAATTCCTTC	CCCTGCGCT	TGATAAAATT	NTNIAAGCCAC	360
CGCAAMCCTY	CGGACCTTC	CTCTKTCGCA	ATYCGRWTCC	RATAYCOCCA	TOGCCCTNKT	420
KYCTYCHICS	GTACCTTAAT	CTGGGTTATO	CTAATANIEYC	CCWAAANMCA	ATCTCTGGGCK	480
KTGCAATKSC	TGGSKTCCG	ATTTAAMMAGA	NGGTTTTCTT	TWTACCAAA	AACCCTNTGG	540
CCCGACACRA	AAAAGKATAA	TAATAKGTG	CHWNCRAAAG	CCGGGGCGCC	RTTTCGAAYC	600
GTGCAACGCC	CCNNGNGTN	AGGTTGGAT	TTTMAACCGC	CAGGCGATTA	SHTTNSGNAA	660
AAACCCCTCN	GGGYMYCAA	AMMCTTTTTC	GGQMTTGTGCG	CCATGKYKCC	AAAACGAAA	720
TTTTTCGCGT	CGWAAAACG	GGCGCCCGG	NGAATTTTTC	GGKACCCCA	ACCGTTTAM	780
CTNNNTTCY	YCCCNACAC	TNGGGGGKHN	NGSSCTNTT	TTTTCYNNAA	GGGGGRGKWC	840
SNCCCONAAN	YCCCNWANG	NGCCCGSNTA	AAAGAGANTT	YCMKAAAAC	CCGCGNCMCC	900
AAAAYACCC	MAAAKWTTC	AAASMSNCNG	YCCCGG			936

(2) INFORMATION FOR SEQ ID NO:331:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1042 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:331:

NGENENKN	ATMMATTCWY	YCTSCACCSG	GGNNNCNATT	GGGGCCRMW	KDTTGTMAAS	60
AGATCTTMAA	YTCGGACACG	ASSSGGACAG	ASCGGGGGG	CTATYCNKCG	GYTGCTCATG	120
CTCACACCG	TCCTCGGGG	GTATAATGG	NCGGCGCGCG	GGCGAACGCG	YTCGAYTGT	180
TCGCGACAC	CATATNCAC	CAAGGTRATA	AAASCACAAAC	CGCGCGCGCG	GGCGCTTGGC	240

SCGGRAASCG	GTGCGCAACCC	RAAACNCCKT	GGGCACYCGG	KTSRACTTTA	AASGGTAATC	300
TCCTCTCT	GGGCTATGGT	GGCCACAAA	CCTSYRGGG	WGCGTCGGC	CCTGGGGYAC	360
CGYCRWTTT	TATNTNTCK	YCTACACNCT	TKGGTYCAG	GAACCCACTT	CACMAAATTC	420
TTTGGGKG	GGGGSGCCCG	YTGTNNCCGK	TAATAATGSG	NTGKTCGGCC	MYCACCGGWA	480
CGTANCTG	GGGGCGCTG	GCRAATTCCT	SAATATCATT	CTTCTGGRAC	CCCCACAMRC	540
CTNAAATTC	GRATCAATNC	CCCNKGCGTT	HTCYCTCTCH	GTTCRCCCAATY	TOGTTCCTAT	600
RKTNCCYAA	TSCAATTTGS	TTYCCRTTSC	YGTSTTCCAA	TTNACACMAE	GTTTTTCTAT	660
ACCAAACCC	NTGGSCCCNA	CNNAAAAAGNA	RAAAANAKGG	KCTTYYAAC	CCCCGGGAT	720
TCAWYGGT	CNENNCCECG	NGKAAGKKGK	GAAYATTHRA	CCCAANACNT	ARATTSGNAR	780
AAACCTYCG	GGGTGMCMAA	MENITWTTSSC	CTTCGGMCTT	YCCAAATMSA	AAATTTYTCY	840
KRMNAAAAMC	YONCCOCSSA	ANATTTTGT	NAAMCCGMA	YTYRTTWWCC	WTITTCGXXC	900
CCMCNNSNC	GNTTCCCTTY	TYATTTCYMM	MCRNNSGACN	CCCCMNTTYY	TWTTCCKWCH	960
MMARGSHNNY	RGGRMMMMNC	CCNCNCNCAS	MCNCNCAAAK	TTTNAACNN	NNKICKCCCC	1020
CCCNMMKNC	CCCNNCMCTT	TM				1042

(2) INFORMATION FOR SEQ ID NO:332:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1073 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:332:

KGNGGOMKKE	ATAMATOWCT	CTSYACCCG	GMTCWATTC	GGCGGMANTC	TNGTMAASAG	60
ATCTCXAATY	CGGCAANAL	ACGCGNAYTC	AACTGTRAYZ	CGGTACACATA	TOMTCGCGNG	120
TCGAGCCCA	AGGCGCTTCA	CGGYCTCCCT	GGGGCGCCAC	GGCATCGGTT	RATGCAACYY	180
CGCGCGCCAC	CGYCAAAAGG	CTCNNTTACG	CGTAAAGGAT	CAMCAATTC	TRAGGTYMCN	240
CACCGTNTTT	GGGGCGCCCG	RAWTYCTAC	CCCGAATWTC	UGTAATCGG	AATTGGGCGW	300
KCGGCGTGGG	CAATGAGKTN	TTGGCGACG	GGCGRWTTC	NTGCGGCGRA	ATTCGCGKAT	360
TCGTTTAACG	GTGTORACCT	TTYCCCGGTT	GGCGTAAATY	YTTCNTGGCC	GGCYTCGGCC	420
CGNACGASY	CTCTAACGGY	CNCCAGGCAA	TACCKTGGC	TTTTRAACCC	CGURATNAAY	480
TCGTTACGAC	YTCGAAAGGT	CTGRANTRTA	TTTCVTRGTA	AANMCCACCN	AACCGGGNTT	540
RATCTGTTTC	MTCANCTTC	SCCGGGTTT	GGCGTTTTC	AAVCTTNTAC	CMTYCAAAAAG	600
GTTCATTTTC	CGAANAAAT	CGGTTTCTCA	CTTGGCCCG	GGCTGGTTT	COMMCCCTTR	660
AMATCCCG	CGCGGAAAG	AMTTGGGTTT	GGCGCGGTTG	CGCGNAATAT	YCTTGCGNCCT	720
GNAAAATGSS	GGGATTCGCG	CGTGNAYCGG	CGTATGGGGGK	TNCGCACTTG	GWACAATTTC	780
WKGCGTTCGA	AAACCGGNC	CGGGGGGTTG	GGCGCGTTTT	CCTMNNNAAA	AAGKGTGTTG	840
WYTTTTGCG	CNEAANTTCA	CGCGCGTAT	GGCGCAACAY	YVYGAANTTC	CAACACTTTA	900
RAAAARANCY	YGTTCYCCG	TTTFTMCCTGG	SAANCCCCG	NMSSSKCGGG	AAAAAAAAGNK	960
TYNGGTTTA	CGSNKTTT	TNTYTCCTCC	NMWRHNSNNY	NCBKKCNKRY	NGNSHMMNCT	1020
WYKTCWNNNN	SGRGGWCKCG	WENCSGKHYM	CNNGCNHNYE	NGNKSNNCCG	MSC	1073

(2) INFORMATION FOR SEQ ID NO:333:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1061 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:333:

GNNNGNNNNNNN	ATMCAYCWY	SCACSGGTC	TATTCGGGCC	GCAATTTGAT	CKASAGATCT	60
CGATTCGCG	AMNNAAARTG	TCTGTCGAA	TTTCGAKKTTG	GTCTTCARAY	GGGCCAGGGC	120
GNGACCRACA	CCCTGNGTCA	CCCAAAANAC	CAACAGCWTG	AAATWTCAAG	GCGRAGUCSC	180
TRTCATACTG	CRASCANTTA	ACCGTTCM	TGAAAGTGTG	CAACAGAGGC	ACCCAGYTC	240
CGGCCSGGCA	ATTCGCGCTG	CGGCCGSGTN	TCAGGCTGAT	TYCTGACCC	RWTCTGTGGG	300
TGGYCAMCT	GTTGAAAGGCC	CGWTCGCGA	AGAACTGGAC	GGCTAATTCC	CAGGACNCIA	360
GRAACCCNAG	GAACCCGCGG	TAKAANCGG	CRAAACCRAG	GGCGYVNGCN	ATTGCAATTAA	420
NAMGGTTT	CRACHTGGC	RAACGTTT	CTTGTTGCGG	CTGGGCAACC	CTGGACCCANT	480
TACCCCGTCTG	CGCGGNGAC	CGCGGTTGCT	TGKYCCCAAT	NTGCYCCCGC	GNRANTNGGC	540
CAAAACCCAG	GGCNCNCACT	TTGCGGCGN	AATTCCYCC	TTTAATCAAC	GGGCNCNCCT	600
GTTTTGGG	AAACCCNCCY	CTTGTGTTAA	CAATCCGCG	AAATGGGNC	TTTGGGAAAT	660
TCTINTYCGG	GGGGCGGCG	AMNYYTCTGT	TCATTCGCG	CTTAMYCCAN	TTCGGSNTCC	720
CGGGCKRAAG	NGGGGGGCGA	AAGGGGCGG	CGGNTISCKC	GGGGKKGCGG	CGGGKTPCAA	780
AANTTGTGG	GTTTGTGCGG	NTTGTGCGG	CGGCAANRA	CGGGGGTTTT	TTTTTGAACC	840
KCMANTGSSA	AMCCCGGSC	CCCAAGGAG	GCCTTAANGG	RAYTTNKGCT	CGNAAACGCG	900
CGGCAKITY	GGGKTKCNC	CGCCGCGKGT	CGMTSTTMM	MRCCCTTGN	GNKTTTPTAN	960
MGSCCTTNNC	CACCGGCGYCK	GGGCKCGMNA	GAATKMYWIC	CNGGGGNWAM	RSCCCCCCIN	1020
GGGGGGGGGG	MGAGYSEKCT	CTKGCGCNCN	YNTTTTCCCG	C		1081

(2) INFORMATION FOR SEQ ID NO:334:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 984 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:334:

GNNNGNNNNNNN	ATMCAYCWY	CTTSCACCGG	GNTGWTGG	GGCGCGAWK	TNGTAAAG	60
ATCTGGAAYT	CGGCACGAG	TGTTGTCGAG	TGTTGTCAG	CTTGTCAACSC	120	
GGTGCCTGCG	JTGTRASCA	CMCATTCGGR	AAATCCTTAAAC	CGGTGCGGCG	GYCACCGGCK	180
TGGCTCTGAA	AACTCTCGG	GGCACCTYCA	AACAAWYCT	CCTGCAACSC	ARSCGCTTTC	240
GGCGGGCAT	CGTGGCGAT	TTGGCGNAG	TTGGCGCCG	GTACTGCGG	CWYCRANACC	300
GCTTGGGCGA	ACCCACGTA	AATGTTGCG	GGTGGCCGAA	GTACTGCGG	CGWYCRANACC	360
TGTTAAACCA	CGGAAACCTY	CGGGCKTCT	CTCTGTCGCA	CCCGCTSCCC	TTRATNATT	420
TGGCTTNTG	KGTYCTKCYG	GTMCCTAAAT	CTTGTTGATG	WTCCGTRWTC	RATNYCGCGA	480
ATCTKGCGT	TCCTATNTGCT	GGGCTTCAA	TTWAMANAG	TATAITGTCG	CTAAATGCGA	540
CCSTTGGGCC	CGAACCAA	AATGATMATA	ATAATGGTGC	CTTCCNAAAC	600	
CGATCGGCK	AMMCCCGC	GGTATKGGG	GNAATTCTTG	TNTCAACCC	CGGCKCGCATY	660
CGAAAACCTY	NCNCMCGGCGA	CGAAAACAY	HTTNTGCGY	AACTCCAAAG	CATAASHTTG	720
CGAAAACCGA	AATACTTNYG	GGYCCAAATA	AMMMSGCGTC	SSNTTGGGNN	YCATGGCTNN	780
KYNAACCCNA	AACCTTTT	CGAACCCDN	WNTTGTCTNC	SAMCCCGAAA	WTTTTTTGTG	840
SSSTTGTCCA	AGTCGKCCMA	AGGGGGRNA	CGCTCCTNCC	RCKCMANTG	CGSGGARTKT	900
TRNAAAAGGG	GKNTYNCMMA	AASCHNCNC	TCCTNNNTN	TKKNCGCGST	AAAGMGTCT	960
NAANASKEYN	NNNNSCCCCC	CGMMNN	AKAMCSCCN	NAAGMGTCT		986

(2) INFORMATION FOR SEQ ID NO:335:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1074 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:336:

NGNGNCNCGT	ATACATCCTT	GATIYACCGN	GGMMNMANTC	CGGCCRMANT	CTNGTMMGASA	60
GATCTTGAAA	YTGGCGGAAAG	AGYATKTCG	GGGGCCAGAT	TINTGGCCCG	CAACCCGCGC	120
ACTTTTGCAAY	TCAACAKTCC	GGGTTGCGCC	AAAANTCCT	ACCCCCATMC	TYCKTGCAAM	180
ASYTGGCGGC	RATTRACACG	CGGGCGGCG	TGCTGGGCCA	GGTATTTCAG	CAGYTCAAY	240
YCTTTTGTAG	TTAAATTCAG	GGGGCGGCCA	GGGGCGGGG	CGGTTKTAGGT	GCCTYCTTC	300
ATMACCACG	CGGGCGGG	CACTTGGCG	AAAATCTCG	GGGTCAACCA	AAATTGCCG	360
CGGGCGAACN	ACCCANCGGA	TYCTGGGTC	AAATYCACCG	GGCCCGGTG	TAAMMMAMMA	420
GRATCTCTG	MANCCCGCCN	TCAGCGSYTHA	CGGCGMACNG	CCGCGCTTGT	CAACCCUCCA	480
RTACCGGGWT	CAACGGCGC	GTCAACATCA	CAAGGGCGCG	AGGGCTCCCG	CGGANSAAAG	540
GTCTTACSCC	TTTAAATTAAC	MAAGTGTGT	TITCGCCCTC	CGAASASNAA	AAACCCCGSC	600
CGGGCCTTCN	NMMGGGTTG	GGGGMANNNN	CGAACCGCGG	CGAACGTC	CGAAAMCTTC	660
CGAGTCNCMT	TTWAAACACN	TTAACACCC	ANTTTTGGGA	AAAGNTTCCC	NTTNYGCCG	720
TTTAAAGKTS	GGGGTYCCTY	TTAAAAAATT	CCCGCRAAAG	CCCCCGGAG	GGTGMAMTCG	780
GGNAAATTTC	CAAMCCNNGK	TTTNTTGGGT	TMCGGGGAA	AAATTYCNCTC	CCYYNNNNGGG	840
CGSSSNNNAT	TTAGGMMNMT	TTTMMMAATM	NSGKNTSAMM	YNNKCCMNIN	SNNSMAMNNK	900
TNAMCNCCN	CTTCNGKNGY	CSCYNGCCSG	GGAGNGGGRAS	MGCGCNAMMA	AYASGNTTNNK	960
CGUGAAMCINN	ARTKCNKNC	CGGGACSMCN	TTTNNMMAATM	CGNCNKCNNN	AAAGGMRACH	1020
CGCNNSNCGM	REGGAATMTH	YCGGGCGGSE	GGKNGKAAAN	GGKNGCGGCG	AAAG	1074

(2) INFORMATION FOR SEQ ID NO:336:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1195 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:336:

NGNGNCNCGT	ATACATCCTT	CTGACCGCGG	GNTMCANTTC	GGCGSCCAWVY	TTGTGCGASAG	50
ATCTTGAAYT	CGGCGANGG	AGCTTCCTCA	CGGCCCCCAG	WACIOTGGCG	TGTGTACCC	120
ATTGCGCGGK	TCACGCGCGG	ATGGACCAK	TNCACGGGG	TCCCGTCCG	CTGCGCCGCG	180
GGGCTTACGG	CGKCTSCWTC	RAAGGGWTG	CGCAACGGCAT	CGGGTTTCT	RAACGCTGGG	240
AAAKTGGCCA	GGCGCTTGTGC	TCAGYGGGT	CGGCCCCCAA	CGCTTCTTCA	300	
AAATCGGGY	TTCTGTYGNC	CTTGAAAYCC	CGGGGSAAGA	ACTGGTTGCG	CGQGAYCTGC	360
TGGAACCTTG	TGAAATACCC	CGANAKTGT	TCTGAMYGC	CGCCGGAAAG	NGAACCTACT	420
TTGNGWANG	TGGCGNCKC	GGCGTTATCA	STCTGTATCA	ACGGGGAACT	GGYGGNNNTTG	480
GGGGAAAAGA	RECTCTAATG	MTYGGTCKCG	OCTOCCGKNC	CGCCCGCTGK	GYCGCNAATG	540
GAAGGCGSMAG	GTTTAANGCC	MTTYCNYCC	ASCGCTSTGA	SGRNWTYYCG	MGAGKAMNN	600
NNKMMAMMGT	TCRGGNGCW	ATSTCGGG	CGTGTAGAGA	AAACTYCCN	WCCGNTNTYSC	660
GAAGGTTKCS	CGCGMTTTS	SCCGMGNANG	YCTGATTGTA	GGGGKGYKCS	CGCGGGGTYTC	720
CGAAGWRYK	CGYAGGGGGM	GNVCSAGCSC	CGMBRATAG	AGNAAGGKTT	RYGSTSKNCC	780
TTTNGGAGC	WSCNCGNSAK	ANAAACNNKAT	TOCSCNTMS	AGHETNKGRT	YCCNKISTTC	840
TAAGAGGAGC	TATKMKCGC	CGTUGGANGMM	GAGGNGCGC	KGCGCGSGRT	TCTNTGNGWAAA	900

TATCAGAGGG	TCGCCGAGGAG	CCCGCTTTTC	TKTQANAAAN	MSSMRKHEKTC	CGGGYCTCTSC	560
GGGTTTTGTA	GAAGTAKTGG	CSCSSENGAC	WCSCMCNNG	AGKQKHTHTNS	YANTGARGCY	1820
MNNSKIMKMT	MSCSCCGCNA	GGAGNGCCG	CSANGMSTG	NEKQNNMSSNG	ARAKGATGG	1880
GGCCNCCNN	MGMGGAAGMGA	SAANGMGGMR	GGGGGKTKGC	TCKCSCCGNS	CSANGRAGAA	1140
GTCTCGSCGC	CGMGGKTYGKT	TKTKTQNETGG	YSTCMESSMM	MAGAAAAGAG	AGGGC	1196

(2) INFORMATION FOR SEQ ID NO:337:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3572 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(3) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:337:

CCATCTGATC	GTGGGCCAAC	AAGCATGGAG	TGGGAACGAT	GCCTCTCATTC	AGCATTTGCA	60
TOGTTTGTTC	AAAACCGGAC	ATGGCACTT	AGTGGCTCTTC	CGCTTCCCGT	ATCGGCGCTGA	120
TTTGATTCG	AGTGAGATAT	TTATGCCAGC	CGACGCCAGC	CAGACCGGCC	GAGACAGAAC	180
TTAAATGGGC	CGGTAACAGC	GGGATTTCGT	GGTGACCCAA	TCGGACCCAGA	TGCTCCRCGC	240
CCAGTCGCT	ACGGCGCTAT	TTGGGAAAGAA	TAATACTGTT	GATGGGTGTC	TGTCAGAGAA	300
CATCAAGAAA	TAACGCGGA	ACATTACTGC	AGGGACACTTC	CACGCAATTC	SCATCCTGTT	360
CATCAGCGG	ATATGTTATG	ATCAGGCCAC	TGACGCCGTT	CUGGAGAAAGA	TTGTOCACCO	420
CGGTTTACG	GGCTTGACG	CGGCTCTGTT	TCTACCTCC	CACCAACCC	CTGGCAACCCA	480
GTGATGCGG	GGGAGATTA	ATGGGCCCGA	GAATTCGGC	CGGGGCGTTC	ACGGGCGAGAC	540
TGGAGGTTGC	AACGCCAATC	AGCAACGACT	GTGGCCCGCC	CAGCTTGTTG	GGCACCGGTT	600
TGGAGATTA	ATTCGATCCTC	GGCTTACCTC	CTTCGACTTC	TCGCGCGTT	TTGCGAGAAA	660
CGTGGCTTC	TTGGGTCGAC	AGGGGGAAN	GGCTTGATGA	AGAGACACCC	SCATACCTTC	720
CGACRTGTA	TAACGTTACT	GGTTTCACAT	TCACCGAATT	GAATTGACTC	TCCTTGGGGC	780
GTATGATC	CATACCCGCA	AGGTTTTG	GGCATTCGAT	GGTGTGCGG	ATCTCGACGC	840
TGTCGTTAT	GGGACTTTG	CTTGGAGG	CGGGCGTAA	TCAGCTTGA	SCCGTTGAGC	900
ACCGCGCGTC	CAAGGATATG	TCATCGAG	GAAGATGGGC	CGCACGTC	CCCGGGCACG	960
GGGGCTTCCA	CGTATGCTTC	GGGAAACAA	GGCGCTTATG	GGCGGAGGTG	GGGAGCCCGA	1020
TCCTGGCCAT	GGGTGATGTC	GGCGTATAG	GGCGCGGCAA	CGCGACCTGT	GGCGCGCGTG	1080
ATGGGGCGCA	CGATGCGCTC	GGCGTAGAGG	ATCGAGATTC	CGATCCCGG	AAATTTAATAC	1140
GAATCTATG	AGGGAAATTC	TTGACGCGTA	AAUAACTCCG	TTAGAAATA	ATTTGGTTTA	1200
ACTTGTAGAA	GGGATGATTC	TTATGGGCG	CGACGATTC	TCGACATTC	1260	
CGGGACGAGC	CGGACATCTT	GGGACACGGG	GGCGGGGAGG	GGGTTTACG	GGGCGCGGGA	1320
TAGCTGCGAT	CGGATCGCG	TCGGCTGGGT	CATTGACGAG	GGATGGCGC	TGGACAGGGC	1380
GGGCAAGATG	ACTTACCGCA	TCAGCTCGA	AGTGTGCTTC	AGAGTGGAGC	GGGGCGACCG	1440
GAGGGGCGTG	AAACACCCAA	GGCGTTTCC	TGAAACGGCG	GGCGCGCGC	GTACTGTGGC	1500
GACTACCGCC	GGCTCGTCG	CGGTGACGTT	GGCGGAGAGC	GGTAGCACCG	TGCTGTACCC	1560
GCTGTTTAC	CTTGCGGGTC	GGGTTTTC	GGAGAGGTAT	CTGAACGTC	GGATTCACGG	1620
TCAGGGGCAAC	GGTTCTGGG	CGCGGATTCG	GCAGGCCGCT	GGCGGAGCG	TCACATCTGG	1680
GGGCTTCCGAC	GGCTATGTTG	CGGAGGTTGA	TATGGCCGGG	CAAGAGGGC	TGATGAAAT	1740
CGGCGCTAGCC	ATCTCGGCTC	AGCAGGTCAA	CTACGACCTG	GGCGGAGTGA	GGGAGCACCT	1800
CAAGCTGAA	GGAAAGATC	GGGGGCGGAT	GTACCGAGG	ACCATCAAA	CTCGGGAGCA	1860
GGCGACGATC	GTGCGCTCA	ACCCGCGGCT	GGACGTGAGG	GGCACCGCG	TAGTTCGCGT	1920
GGCACCGCTC	GGGGGTCG	GTGACACTT	CTTGGTGG	GGACGCGCG	GGATTCACGG	1980
TGGCGAGGGC	TGGGGCAACT	CGGGCGGCTT	GGGACGAC	CTGGACATTTC	GGCGCGTCCC	2040
GGGTGCGCTG	GGTGAAGACO	GGACGCGGCG	CATGTYGAAC	GGTGGCGCG	AGAACACGCG	2100
CTGGGTGGCC	TATATGGGA	TCAGCTTCTT	CGACCGAGG	AGTGAACGGG	GGTGGGGCGA	2160
GGCCGAACTA	GGGAAATCT	CTTGCAATT	TTTGTGCGG	GGACGCGCGA	GGATTCACGC	2220

CCGGCGGGCT	GGCTTCUCAAT	CGAAAACCCC	GGCGAAACCG	GGCTATTGCGA	TGATTCGACGG	3280
GCCCCCCCCC	GACGCTTCAAC	CGATCTCAAA	CTACGGACTAC	GGCATCTGTC	ACAAACCGGCA	2140
AAAGGACGCC	GGACCCGGCGC	AGACCTTCTCA	GGCATTTTCTG	CACTGGCGCA	TCAACCGGCG	2400
CAACAAAGGC	GGTTGCTCTG	ACGGATTTCA	TTTCGGACCGG	CTGGCGCCCG	CGCTGGTGGAA	2460
GTGTTCTGAC	GGCTTGTATGG	CGACGATTTG	CAGGCUCTGAG	ATGAAGACCG	ATGCCGCTTAC	2520
CTTGGCGGCG	GGACGCAATTA	ATTCGGACG	GGATCTCGGC	GGCTGAAAGG	CCACGATGAGA	2580
CGGAGTGGAG	CTGGACGGCG	GGTGGTGGCA	GGGGCACTGG	CGGGGGCGCG	CGGGGGAGCGC	2640
CGCCGAGGGC	GGCTGGTGGTGC	GGTCCAAAGA	AGCAGGCAAT	ANGCAGAAAGC	AGGAACTGAA	2700
CGAGATCTCG	GGAGGATTTG	GTGAGGGCGG	CGTGGCAATC	TGGAGGCGGC	ACCGAGGACCA	2760
GGACGAGGGC	GGTGGCTGGC	AAATGGGGCT	GGTGGTCAAGC	TTGGCGCTGC	CTGCTGGCTG	2820
GGTGGAGCTT	GGACGCGGGCG	ACCTGGACTA	CGGTTGAGCA	CTGCTCGAGCA	AAACACCGGG	2880
GGAGCTCCCA	TTTGGCGGAC	AGGGCGGCCG	GGGGCGGAA	GGACGCGGAA	TGGGCTCTCG	2940
CGCGCTAGAC	CGAAAGCTTT	AGGGCAGGCG	GGAGGGACCC	GACTCCAAGG	CGGGGGCGCG	3000
GGTGGGCTCG	GACATGGGTT	ATTTCTATAT	GGCCCTAACCG	GGGACCCGGG	TGACCAAGGA	3060
AAAGCTCTTC	CTTGGACGCCA	AGGGGGGTTG	TGGAAAGGGCG	TGTTTATTGAC	AAAGTCAGTT	3120
CGGGCATCCG	AGTAAGGGCGA	AGGGCGGAGAT	CTGGACGGCG	GTAACTCGGT	CGCCCGCGCG	3180
GAACGCACCG	GGACGCCCGGC	CGGCTGACCG	CTGGGGTTGG	TGATGGCTCG	GGACCCCGAA	3240
GAACGGGGTG	GGACGGGGCG	GGGGCAAGGG	GGTGGCGGAA	TGGATCCGGG	CTTGGCTCG	3300
CGGGGGCGCG	GGCTGGCGG	GGGAAGGGTCC	TTCTACGGGG	ACGGACCGGG	CACCCGGCGG	3360
GACCTTACCG	GGCTTGGAGAT	TGGCGATGAA	TCGATCACAC	TCGGGGCGCG	TGGAGGACAA	3420
CGACCAACCG	CACTGGAGATG	GGCTTGCTAA	CAAAAGGGCGA	AGGGAAAGCT	AGTTGGCTGC	3480
TGGCGACGCT	GGACGAAATAC	TGGCTAAACG	CTTGGGGGGG	TCTAAACGGG	TCTTGAAGGGC	3540
TTTTTGTGTC	AAAGGAGGGAA	CTATACCGG	AT			3520

102 INFORMATION FOR SEC IN NO: 338.

50 SCIENCE CHARACTERISTICS.

- (A) LENGTH: 20 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

MOLECULAR MODEL peptide

(84) SEQUENCE DESCRIPTION: SEQ ID NO:128:

Val Gln Phe Gln Ser Gly Gly Asp Asn Ser Pro Ala Val Tyr Xaa Xaa
 1 5 10 15
 Asp Gly Xaa Arg 20

(2) INFORMATION FOR SBC 880 IN NO. 338-

1.2 SEQUENCE CHARACTERISTICS

- (A) LENGTH: 10 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

ANSWER: NO

(X4) SEQUENCE DESCRIPTION: SEQ ID NO:118

Thr Thr Val Pro Lys Val Thr Glu Ala Arg

(2) INFORMATION FOR SEQ ID NO:340:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:340:

Thr Thr Pro Ser Xaa Val Ala Phe Ala Arg
1 5 10

(2) INFORMATION FOR SEQ ID NO:341:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 12 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:341:

Aap Ala Gly Xaa Ala Gly Xaa Asp Val Xaa Arg
1 5 10

(2) INFORMATION FOR SEQ ID NO:342:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:342:

Thr Xaa Glu Glu Xaa Glu Ser Phe Asn Ser Ala Ala Pro Gly Asn
1 5 10 15
Xaa Lys

(2) INFORMATION FOR SEQ ID NO:343:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Other

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:343:

CTAGTTAGTA CTCAGTCGCA GACCCGTG

27

(2) INFORMATION FOR SEQ ID NO:344:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Other

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:344:

GCAGTGACGA ATTCATCTTG ACTCC

28

(2) INFORMATION FOR SEQ ID NO:345:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2412 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:345:

CATATGGGCC	ATCATCATCA	TCATCACCTT	ATCGACATCA	TGGGGGACAG	CCGCACATCC	60
TCGGAAACAGG	CGGCAGCGCGA	GGCGCTTCAAG	CGGGCGCGCG	ATAGCCTGCA	TGACATCGC	120
GTGCGCTCGG	TCATTCGAGGA	GGACATGGCC	GTGGACAGCG	CCGCACAGAT	CACCTACCGC	180
ATCAGACCTG	AAAGTGCTTT	CAAGATGAGG	CGGGCGCAAC	CGAGGGGCTG	GAACACCGCG	240
AGCGGTTTGG	CTGAAACAGG	CGCCCGCGCC	GGTACTCTTG	CGACTACCCC	CGCGCTCGCG	300
CGGGCTGAGT	CGGGCGAGGC	CGTAAACACG	CTCTCTTACT	CGCTGTTCGA	CGTGTGCGGT	360
CGGGGCTTC	ACGAGAGGTA	TGCGAACCTC	ATGATGACCG	CTCAAGGGAC	CGGTGCTGCT	420
CGCGGATAGG	CGCGAGCGCG	CGCGCGGACG	GTCAACATG	GGGCGCTCCGA	CGCCCTATCTG	480
TCGGAGGTTG	ATATGCGCCG	SCAACAGGGG	CTGATGAGCA	TCCCGCTATGC	CATCTCCGCT	540
CAGCAGGTC	ACTACACAGT	GCCTGGAGTG	AGCGGNGCAGC	TCAAGCTGAA	CGGAAAAGTC	600
CTGGGGGGCA	TGTACCTGGG	TCACCATGAA	ACCTGGGAGC	ACCGCGAGAT	CGCTGCGCTC	660
AACCCCGGGG	TGAACCTGGC	CGCGACCTGC	GTAGTTCGCG	TGCAACGGTC	CGACGGGTCC	720
GGTGACACCT	TCTTGTTCAC	CGCACTACTG	TCCAAAGCA	ATCCCGAGGG	CTGGGGCAAG	780
TGCCCCGGGT	TGGCGCCAC	CGTGGACTTC	CGGGGGGTG	CGGCGTGCCT	GGTGTGAAAC	840
GGCAACCGCG	GCATGGTGTAC	CGTGGCGCT	GAGACACCGG	GTGCGCTGGC	CTATATCGC	900
ATCAGCTTCC	TCGACCGCGC	CGTGTACACG	GGACTCGCGG	AGGCCCAACT	ACGCAATAGC	960
TGTGGCAATT	TGTGTTCTGC	CGAGCGCGAA	ACGATTCAGG	CCCGCGCGCG	TGGCTTGCAC	1020
TOGAAACGGG	CGCGCAACAA	GGGATTCTG	ATGATGAGC	GGCGCGCCCG	GGACGGGTAC	1080
CGGATCATCA	ACTACAGCTA	CGCGATGTC	AACAAACCGG	AAAAGGGACCG	CUCGACCGCG	1140
CAGGCTCTGC	AGGCAATTCTT	GCATGCGGCG	ATGACCGAGC	GCAGACAAAGC	CTGTTTCTC	1200
CAGCGATGTC	ATTCGCGGCC	GTGCGCGCGC	GGCGTGTGTA	AGTTGTTGTA	CGCGTTGATC	1260
CGCGGATTT	TCAGCGCGCC	GTAGGAGACG	GATGCGCGTA	CGCTCGCGCA	GGAGCGAGGT	1320

AATTCGAGC	CGATCTCGG	CGACCTGAA	ACCCAGATCG	ACCAAGTGG	GTGACAGCA	1380
GGTCGTTGC	AGGCCGATG	GGCGGCGCG	CGCGGACGCG	CGCGCCAGGC	CGCGGTGTTG	1440
CGCTTCCAG	AAGCAGCCAA	TAAGCAGAAAG	CAGGAACCG	ACGAAATTC	GAAGAAATTG	1500
CGTCAGGGCG	CGCTGCAATA	CTCGAAGGCG	GAACGAGGAGC	AGCACGAGGC	GCTGTCCTCG	1560
CAATAGGGCT	TTGTGCCCCAC	AACCGGGCGT	TCGCCCCCGT	CGACCGCTGC	AGCGCCACCC	1620
GCACCGGGCGA	CACCTGTTGC	CCCCCGACCA	CCCGCGCGCG	CCACACCGCG	GAATGCCCG	1680
CGGGGGGCGATC	CCACCGGAGC	ACCTCGCCCG	CGCGACCCCGA	ACGACACCGG	CCACCTGTC	1740
ATTCGGCCCA	ACGCAACCCA	ACCTTCGCG	ATCGACAAACC	CGGTGGAGG	ATTCAGCTTC	1800
GGCGTGGCTG	CTGCGCTGGT	GGAGCTGAC	GGCGGCCACT	TGAGTAAAG	TTGAGCAGTC	1860
CTCACGAA	CCACCGGGGA	CCCGCCRTT	CCCGACACAGC	CCCGCCCGGT	GGCCAAATGAC	1920
ACCCGATAC	TGCTCGCGCG	GTAGACARA	AACTTGTAC	CCAGCGCCGA	AGCCACCGAC	1980
TGAAAGGGCG	CGCGCGCGGT	GGGTCTCGAC	ATGGGTGAGT	TCTATATGCU	CTACCCCGGC	2040
ACCCGCGATC	ACCGGAAAC	GTCTCTGCTC	GACGCCAAGC	GGGTGTCG	AAGCCGCTCG	2100
TATTAAGGAG	TCAGATTCAG	CGATCCGAGT	AACCGGAAACG	GGCAGATCTG	GACGGCGTGA	2160
ATCGGCTGG	CGGGCGGCAA	CGCACCGACG	GGCGGGCGCG	CTGAGCTGTC	GTITTTGGTGA	2220
TGGCTGGGA	GGCCAAACAA	CCCGGTGAC	AAAGGGCGGG	CCAGGGCGT	GGCCGATCG	2280
ATCCGGGCTT	TTGGTGGCGG	GGCGGGCGCG	CGCGCACCGG	CTGCTGAGA	GGCGGTCTCG	2340
GGCGCCGGCG	CGGGCGGGGA	AGTCGCTCT	ACCGGAGGCA	CACTGACACC	CGACGCGACC	2400
TTACCGGCGCT	GA					2412

(2) INFORMATION FOR SEQ ID NO:346:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 802 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:346:

Met	Gly	His	Gly	His	Gly	His	Gly	His	Val	Ile	Asp	Ile	Ile	Gly	Thr	Ser
1									5	10	15					
Pro	Thr	Ser	Trp	Glu	Gln	Ala	Ala	Glu	Ala	Val	Gln	Arg	Ala	Arg		
									20	25	30					
Asp	Ser	Val	Asp	Asp	Ile	Arg	Val	Ala	Arg	Val	Ile	Glu	Gln	Asp	Met	
									35	40	45					
Ala	Val	Asp	Ser	Ala	Gly	Lys	Ile	Thr	Tyr	Arg	Ile	Lys	Leu	Gln	Val	
									50	55	60					
Ser	Phe	Lys	Met	Arg	Pro	Ala	Gln	Pro	Arg	Gly	Ser	Lys	Pro	Pro	Ser	
									65	70	75					
Gly	Ser	Pro	Glu	Thr	Gly	Ala	Gly	Ala	Gly	Thr	Val	Ala	Thr	Thr	Pro	
									85	90	95					
Ala	Ser	Ser	Pro	Val	Thr	Leu	Ala	Glu	Thr	Gly	Ser	Thr	Leu	Leu	Tyr	
									100	105	110					
Pro	Leu	Phe	Asn	Leu	Trp	Gly	Pro	Ala	Phe	His	Glu	Arg	Tyr	Pro	Asn	
									115	120	125					
Val	Thr	Ile	Thr	Ala	Gln	Gly	Thr	Gly	Ser	Gly	Ala	Gly	Ile	Ala	Gln	
									130	135	140					
Ala	Ala	Ala	Gly	Thr	Val	Asn	Ile	Gly	Ala	Ser	Asp	Ala	Tyr	Leu	Ser	
									145	150	155					
Gln	Gly	Asp	Met	Ala	Ala	His	Lys	Gly	Leu	Met	Asn	Ile	Ala	Leu	Ala	
									160	165	170					
Thr	Ser	Ala	Gln	Ser	Val	Asn	Tyr	Asn	Leu	Pro	Gly	Val	Ser	Glu	His	

180	185	190
Leu Lys Leu Asn Gly Lys Val Leu Ala Ala Met Tyr Gln Gly Thr Ile		
195	200	205
Lys Thr Trp Asp Asp Pro Gln Ile Ala Ala Leu Asn Pro Gly Val Asn		
210	215	220
Leu Pro Gly Thr Ala Val Val Pro Leu His Arg Ser Asp Gly Ser Gly		
225	230	235
Asp Thr Phe Leu Phe Thr Gln Tyr Leu Ser Lys Gln Asp Pro Gln Gly		240
245	250	255
Trp Gly Lys Ser Pro Gly Phe Gly Thr Thr Val Asp Phe Pro Ala Val		
260	265	270
Pro Gly Ala Leu Gly Glu Asn Gly Asn Gly Met Val Thr Gly Cys		
275	280	285
Ala Glu Thr Pro Gly Cys Val Ala Tyr Ile Gly Ile Ser Phe Leu Asp		
290	295	300
Gln Ala Ser Gln Arg Gly Leu Gly Gln Ala Gln Leu Gly Asn Ser Gln		
305	310	315
Gly Asn Phe Leu Leu Pro Asp Ala Gln Ser Ile Gln Ala Ala Ala Ala		320
325	330	335
Gly Phe Ala Ser Lys Thr Pro Ala Asn Gln Ala Ile Ser Met Ile Asp		
340	345	350
Gly Pro Ala Pro Asp Gly Tyr Pro Ile Ile Asn Tyr Glu Tyr Ala Ile		
355	360	365
Val Asn Asn Arg Gln Lys Asp Ala Ala Thr Ala Gln Thr Leu Gln Ala		
370	375	380
Phe Leu His Trp Ala Ile Thr Asp Gly Asn Lys Ala Ser Phe Leu Asp		
385	390	395
Gln Val His Phe Gln Pro Leu Pro Pro Ala Val Val Lys Leu Ser Asp		400
405	410	415
Ala Leu Ile Ala Thr Ile Ile Ser Ser Ala Glu Met Lys Thr Asp Ala Ala		
420	425	430
Thr Leu Ala Gln Glu Ala Gly Asn Phe Glu Arg Ile Ser Gly Asp Leu		
435	440	445
Lys Thr Gln Ile Asp Gln Val Glu Ser Thr Ala Gly Ser Leu Gln Gly		
450	455	460
Gln Trp Arg Gly Ala Ala Gly Thr Ala Ala Gln Ala Ala Val Val Arg		
465	470	475
Phe Gln Glu Ala Ala Asn Lys Gln Lys Glu Glu Leu Asp Glu Ile Ser		480
485	490	495
Thr Asn Ile Arg Gln Ala Gly Val Gln Tyr Ser Arg Ala Asp Glu Glu		
500	505	510
Gln Gln Gln Ala Leu Ser Ser Gln Met Gly Phe Val Pro Thr Thr Ala		
515	520	525
Ala Ser Pro Pro Ser Thr Ala Ala Ala Pro Pro Ala Pro Ala Thr Pro		
530	535	540
Val Ala Pro Pro Pro Pro Ala Ala Ala Asn Thr Pro Asn Ala Gln Pro		
545	550	555
Gly Asp Pro Asn Ala Ala Pro Pro Pro Ala Asp Pro Asn Ala Pro Pro		560
565	570	575
Pro Pro Val Ile Ala Pro Asn Ala Pro Gln Pro Val Arg Ile Asp Asn		
580	585	590
Pro Val Gly Gly Phe Ser Phe Ala Leu Pro Ala Gly Trp Val Glu Ser		
595	600	605
Asp Ala Ala His Phe Asp Tyr Gln Ser Ala Leu Leu Ser Lys Thr Thr		
610	615	620

Gly Asp Pro Pro Phe Pro Gly Gln Pro Pro Pro Val Ala Asn Asp Thr
 625 630 635 640
 Arg Ile Val Leu Gly Arg Leu Asp Gln Lys Leu Tyr Ala Ser Ala Glu
 645 650 655
 Ala Thr Asp Ser Lys Ala Ala Arg Leu Gly Ser Asp Met Gly Glu
 660 665 670
 Phe Tyr Met Pro Tyr Pro Gly Thr Arg Ile Asn Gln Glu Thr Val Ser
 675 680 685
 Leu Asp Ala Asn Gly Val Ser Gly Ser Ala Ser Tyr Tyr Glu Val Lys
 690 695 700
 Phe Ser Asp Pro Ser Lys Pro Asn Gly Gln Ile Trp Thr Gly Val Ile
 705 710 715 720
 Gly Ser Pro Ala Ala Asn Ala Pro Asp Ala Gly Pro Pro Gln Arg Trp
 725 730 735
 Phe Val Val Trp Leu Gly Thr Ala Asn Asn Pro Val Asp Lys Gly Ala
 740 745 750
 Ala Lys Ala Leu Ala Glu Ser Ile Arg Pro Leu Val Ala Pro Pro Pro
 755 760 765
 Ala Pro Ala Pro Ala Pro Ala Glu Pro Ala Pro Ala Pro Ala Pro Ala
 770 775 780
 Gly Glu Val Ala Pro Thr Pro Thr Pro Thr Pro Gln Arg Thr Leu
 785 790 795 800
 Pro Ala

(2) INFORMATION FOR SEQ ID NO:347:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 34 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(iii) MOLECULE TYPE: Other

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:347:

GGATCCAAAC CACCGAGCGG TTCCGCTGAA ACGG

34

(2) INFORMATION FOR SEQ ID NO:348:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 37 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(iii) MOLECULE TYPE: Other

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:348:

CGCTGCGAAT TCACTCCCGG AGGAAATCGT CGCGATC

37

(2) INFORMATION FOR SEQ ID NO:349:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1962 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(11) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:349:

CTATATGGCC	ATCATCATCA	TCATACCGGA	TGAAACACAC	CGACCGTTC	GGCTGAAGAC	60
GGCGCGCGCG	CGGTTACTCT	GGCACTTAC	CGCGCTGCGT	CGCGCGTAC	GTGCGCGAG	120
ACCGTGTAGCA	CGCTGTCTTA	GGCGGTCTTA	ACCTGTGGGG	GTGCGCGCTT	TCACCGAGG	180
TATCCCGAACG	TCAGATCATC	GGTCAGGGCG	ACCGGTTCTG	GTGCGCGGAT	CGCGCGAGGC	240
GGCGCGCGGA	CGGTCAACAT	TGGGCGCTTC	GAACGTTATC	TGTGCGAGG	TGATATGGCA	300
GGCGCAAGG	GGCTGAAGAA	CATCGCGCTA	GGCATCTCGG	CTGACGAGT	CAACTACAC	360
CTGCGCTGGAG	TGAGCGAGCA	CGTCACGCTA	ACGCGAAAAC	TCTGCGCGC	CATGTACCG	420
GGCACTCATCA	AAACGTTGGAA	CGACCCCGAA	ATGCGTGGCG	TCACCGGGG	CGTGAACTG	480
CGCGCGCAACG	CGGTMTTCTG	CGTGACCGCC	TCGCGACGCT	CGCGTGAAC	CTTCCTGTTG	540
ACCCGTTACG	TGTGCGAGGAA	AGATCGCCCG	GGCTGGGCGA	AGTCGCGCG	CTTGGCGACT	600
ACCGTGTACT	TCCCGCGCGT	CGCGGGTGC	CTGGGTGAGA	ACGCGAACG	CGCGCATGTC	660
ACCGTGTACT	CGGCGTGTGTT	CGCTTATACG	CGCATCGCTT	CTTGACGCTT	CTTGACCGAC	720
CGCACTAAC	GGGGACTCTG	CGAAGCGCTA	CTGAGCGATA	GCTCTGGCGA	TTCCTGTTTG	780
CGGAGCGCG	RAAGCTTCA	GGCGCGCGCG	CGTGGCGCTG	CATCGAAAAC	CGCGCGGAC	840
CAGGGCAATTG	CGATGATGAA	CGGGCGCGCG	ACCGGACGCT	ACCGGATCAT	CAACTACCGA	900
TACCGCTTCA	TCACACACCG	CGCAAAAGAC	CGCGCGTACT	CGCAGACGTT	CGACGCGATT	960
TGAGACTGGG	CGTACCGCGA	CGGCGAACAG	CGCTGGCTG	TCGACGAGT	TCATTTGGAG	1020
CGCGCGCGCG	CGCGCGTGTG	GAAGTGTGTT	GAAGGTTGTA	TCGGGAGAT	TCCTCTCGGA	1080
GGTGCGACTG	GGGGGCGCTG	AGGTGGAGGT	TCTGGCGGA	CGTGGCGCG	ACCGGCGCGCC	1140
TGGCGCGCGT	GGGACTCTCA	AGGCGCGACG	CGACCGCGCG	CGTGGCGCG	CGCGCGCGAC	1200
CGGGCGCGCG	TCACACACCG	GAATCCCGAG	CGGCGCGCG	CGACCGCGAC	ACCGTGGCGCG	1260
CGCGACCGCGA	ACCGGCGCG	ACCGGCGTGT	ATTCGCGCGA	ACCGGCGCGA	ACCGTGTGCG	1320
ATCGACAACT	CGGTTTGGAG	ATTCGCGCTG	CGCTGGCTG	CGACTGTGAC	CGACTGTGAC	1380
CGCGCGCGAC	TCGACTTACG	TCGACGACG	CTTACGAAAAA	CGACCGCGCG	CGCGCGCGATT	1440
CGCGCGACAG	CGGCGCGCG	CGGCGCGCG	CGGCGCGCG	TCGTCGGCG	CGTAGACCGA	1500
AAGCTTACG	CGACCGCGCG	AAGGACCGTAC	TCGAAGGGCG	CGGCGCGCG	CGGCTCGCG	1560
ATGGGGTGTG	TCTTATGCTG	CTACCGGGCG	ACCTGGATCA	ACGAGGAAAC	CGTGTGCGTC	1620
GAACCGAACG	CGGTGCGTGTG	AAGGCGCTG	ATTCAGCGAG	TCAGGTTGAG	CGATCGCGAT	1680
AAAGCGAACG	GGCGTGTGCG	CGACGGCGTA	ATTCGCGCG	CGGGGGGCGA	CGACCGCGAC	1740
CGCGCGCGCG	CTGAGCGCTG	GGTTTGTGTA	TCGCTCGCGA	CGCGCGACAA	CGCGCGCGAC	1800
AAAGCGCGCG	GGCGTGTGCG	GGCGTGTGCG	ATCGCGCGCT	GGTGGCGCG	CGCGCGCGCG	1860
CGGGCGCGCG	CTGCTCGCGA	GGCGTGTGCG	GGCGCGCGCG	GGCGCGCGCG	AGTCGCGCT	1920
ACCGGCGCGA	ACCGGCGACG	GGCGTGTGCG	GA			1982

(12) INFORMATION FOR SEQ ID NO:350:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 531 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(13) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:350:

Met Gly His His His His His His Gly Ser Lys Pro Pro Ser Gly Ser
 1 8 10 13
 Pro Glu Thr Gly Ala Gly Ala Gly Thr Val Ala Thr Thr Pro Ala Ser
 20 25 30
 Ser Pro Val Thr Leu Ala Glu Thr Gly Ser Thr Leu Leu Tyr Pro Leu
 35 40 45
 Phe Asn Leu Trp Gly Pro Ala Phe His Glu Arg Tyr Pro Asn Val Thr
 50 55 60
 Ile Thr Ala Gln Gly Thr Gly Ser Gly Ala Gly Ile Ala Gln Ala Ala
 65 70 75 80
 Ala Gly Thr Val Asn Ile Gly Ala Ser Asp Ala Tyr Leu Ser Glu Gly
 85 90 95
 Asp Met Ala Ala His Lys Gly Leu Met Asn Ile Ala Leu Ala Ile Ser
 100 105 110
 Ala Gln Gln Val Asn Tyr Asn Leu Pro Gly Val Ser Glu His Leu Lys
 115 120 125
 Leu Asn Gly Lys Val Leu Ala Ala Met Tyr Glu Gly Thr Ile Lys Thr
 130 135 140
 Trp Asp Asp Pro Gln Ile Ala Ala Leu Asn Pro Gly Val Asn Leu Pro
 145 150 155 160
 Gly Thr Ala Val Val Pro Leu His Arg Ser Asp Gly Ser Gly Asp Thr
 165 170 175
 Phe Leu Phe Thr Gln Tyr Leu Ser Lys Glu Asp Pro Glu Gly Trp Gly
 180 185 190
 Lys Ser Pro Gly Phe Gly Thr Thr Val Asp Phe Pro Ala Val Pro Gly
 195 200 205
 Ala Leu Gly Glu Asn Gly Asn Gly Gly Met Val Thr Gly Cys Ala Glu
 210 215 220
 Thr Pro Gly Cys Val Ala Tyr Ile Gly Ile Ser Phe Leu Asp Glu Ala
 225 230 235 240
 Ser Glu Arg Gly Leu Gly Glu Ala Gln Leu Gly Asn Ser Ser Gly Asn
 245 250 255
 Phe Leu Leu Pro Asp Ala Gln Ser Ile Gln Ala Ala Ala Ile Ala Gly Phe
 260 265 270
 Ala Ser Lys Thr Pro Ala Asn Gln Ala Ile Ser Met Ile Asp Gly Pro
 275 280 285
 Ala Pro Asp Gly Tyr Pro Ile Ile Asn Tyr Glu Tyr Ala Ile Val Asn
 290 295 300
 Asn Arg Gln Lys Asp Ala Ala Thr Ala Gln Thr Leu Gln Ala Phe Leu
 305 310 315 320
 His Trp Ala Ile Thr Asp Gly Asn Lys Ala Ser Phe Leu Asp Glu Val
 325 330 335
 His Phe Gln Pro Leu Pro Pro Ala Val Val Lys Leu Ser Asp Ala Leu
 340 345 350
 Ile Ala Thr Ile Ser Ser Gly Gly Ser Gly Gly Ser Gly Gly
 355 360 365
 Gly Ser Gly Gly Ser Val Pro Thr Thr Ala Ala Ser Pro Pro Ser Thr
 370 375 380
 Ala Ala Ala Pro Pro Ala Pro Ala Thr Pro Val Ala Pro Pro Pro Pro
 385 390 395 400
 Ala Ala Ala Asn Thr Pro Asn Ala Gln Pro Gly Asp Pro Asn Ala Ala
 405 410 415
 Pro Pro Pro Ala Asp Pro Asn Ala Pro Pro Pro Pro Val Ile Ala Pro
 420 425 430

Asn Ala Pro Gln Pro Val Arg Ile Asp Asn Pro Val Gly Gly Phe Ser
435 440 445
Phe Ala Leu Pro Ala Gly Trp Val Glu Ser Asp Ala Ala His Phe Asp
450 455 460
Tyr Gly Ser Ala Leu Leu Ser Lys Thr Thr Gly Asp Pro Pro Phe Pro
465 470 475 480
Gly Gln Pro Pro Pro Val Ala Asn Asp Thr Arg Ile Val Leu Gly Arg
485 490 495
Leu Asp Gln Lys Leu Tyr Ala Ser Ala Glu Ala Thr Asp Ser Lys Ala
500 505 510
Ala Ala Arg Leu Gly Ser Asp Met Gly Glu Phe Tyr Met Pro Tyr Pro
515 520 525
Gly Thr Arg Ile Asn Gln Glu Thr Val Ser Leu Asp Ala Asn Gly Val
530 535 540
Ser Gly Ser Ala Ser Tyr Tyr Glu Val Lys Phe Ser Asp Pro Ser Lys
545 550 555 560
Pro Asn Gly Gln Ile Trp Thr Gly Val Ile Gly Ser Pro Ala Ala Asn
565 570 575
Ala Pro Asp Ala Gly Pro Pro Gln Arg Trp Phe Val Val Trp Leu Gly
580 585 590
Thr Ala Asn Asn Pro Val Asp Lys Gly Ala Ala Lys Ala Leu Ala Glu
595 600 605
Ser Ile Arg Pro Leu Val Ala Pro Pro Pro Ala Pro Ala Pro Ala Pro
610 615 620
Ala Glu Pro Ala Pro Ala Pro Ala Pro Ala Gly Glu Val Ala Pro Thr
625 630 635 640
Pro Thr Thr Pro Thr Pro Gln Arg Thr Leu Pro Ala
645 650

PATENT COOPERATION TREATY

PCT

DECLARATION OF NON-ESTABLISHMENT OF INTERNATIONAL SEARCH REPORT
(PCT Article 17(2)(a) and Rule 39)

Applicant's or agent's file reference 9532-023-228	IMPORTANT DECLARATION		Date of mailing (day/month/year) 22 JUNE 1999
International application No. PCT/US99/028265	International filing date (day/month/year) 17 FEBRUARY 1999	(Earliest) Priority Date (day/month/year) 18 FEBRUARY 1998	
International Patent Classification (IPC) or both national classification and IPC Please See Continuation Sheet.			
Applicant CORIXA CORPORATION			

This International Searching Authority hereby declares, according to Article 17(2)(a), that no international search report will be established on the international application for the reasons indicated below.

1. The subject matter of the international application relates to:
 - a. scientific theories.
 - b. mathematical theories.
 - c. plant varieties.
 - d. animal varieties.
 - e. essentially biological processes for the production of plants and animals, other than microbiological processes and the products of such processes.
 - f. schemes, rules or methods of doing business.
 - g. schemes, rules or methods of performing purely mental acts.
 - h. schemes, rules or methods of playing games.
 - i. methods for treatment of the human body by surgery or therapy.
 - j. methods for treatment of the animal body by surgery or therapy.
 - k. diagnostic methods practiced on the human or animal body.
 - l. mere presentations of information.
 - m. computer programs for which this International Searching Authority is not equipped to search prior art.
2. The failure of the following parts of the international application to comply with prescribed requirements prevents a meaningful search from being carried out:

the description the claims the drawings
3. The failure of the nucleotide and/or amino acid sequence listing to comply with the prescribed requirements prevents a meaningful search from being carried out:

it does not comply with the prescribed standard
 it is not in the prescribed machine readable form

4. Further comments:

Name and mailing address of the ISA/US
Commissioner of Patents And Trademarks
Box PCT
Washington, D.C. 20231

Fax number (703) 308-4329

Form PCT/ISA/203 (July 1992)*

Authorized office

Field-Collins, Jr.
MICHAEL WOODWARD

Telephone No. (703) 308-4028

**DECLARATION OF NON-ESTABLISHMENT OF
INTERNATIONAL SEARCH REPORT**

International application No.
PCT/US99/03265

The International Patent Classification (IPC) or National Classification and IPC are as listed below:

IPC(5): A61K 38/00; C07K 1/00; C07K 16/00; C12Q 1/68; C12P 19/34; C07H 21/02, 21/04
US Cl. 530/300, 350, 387.1; 435/6, 91.1, 91.2, 536/23.1, 24.3, 24.31, 24.32, 24.33